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(54) **IDENTIFICATION OF TUMOR-ASSOCIATED MARKERS FOR DIAGNOSING OR MONITORING OVARIAN CANCER**

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C07H 21/04	(2006.01)
C07K 16/30	(2006.01)
C07K 14/47	(2006.01)

(52) **U.S. Cl.**
CPC *C07K 16/30* (2013.01); *C07K 14/4748* (2013.01); *C12Q 1/6886* (2013.01); *C12Q 2600/158* (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

5,990,299	A *	11/1999	Ruzdijic et al.	....	536/24.5
7,371,840	B2 *	5/2008	Press et al.	....	536/23.5
2002/0086356	A1	7/2002	Tuschl		
2003/0099974	A1	5/2003	Lillie et al.		
2003/0148410	A1 *	8/2003	Berger et al.	....	435/7.23
2004/0005563	A1	1/2004	Mack et al.		
2007/0037204	A1	2/2007	Aburatani et al.		
2007/0099251	A1 *	5/2007	Zhang et al.	....	435/7.23
2008/0153104	A1 *	6/2008	Aburatani et al.	....	435/7.1
2009/0214550	A1	8/2009	Sahin et al.		

FOREIGN PATENT DOCUMENTS

JP	2005/500833 A	1/2005
JP	2007506417 A	3/2007
JP	2007/526759 A	9/2007
WO	92/04381 A1	3/1992
WO	96/33265 A1	10/1996
WO	96/33739 A1	10/1996
WO	0194641 A2	12/2001
WO	02/102235 A2	12/2002
WO	03/065006 A1	8/2003
WO	2005113587 A2	12/2005
WO	2006083986 A2	8/2006
WO	2006100089 A2	9/2006
WO	2007031222 A2	3/2007

OTHER PUBLICATIONS

Schmidt et al. Blood. 1998. 91: 22-29.*
Garber et al. PNAS. 2001. 98: 13784-13789.*
Bhattacharjee et al. PNAS. 2001. 98:13790-13794.*
Ito et al. AntiCancer Research. 2002. 22(4):2385-2389.*
Dermer, G.B. Bio/Technology (1994) 12: 320.*
Liu et al. Clinical Immunology. 2004. 112: 225-230.*
Coleman, R. Drug Discovery Today. 2003. 8: 233-235.*
Saetre et al. Molecular Brain Research. 2004. 126: 198-206.*
Hanke et al. Clinical Chemistry. 2007. 53: 2070-2077.*
Palmer et al. BMC Genomics. 2006. 7:115.*
Min et al. BMC Genomics. 2010. 11:96.*
Mitsuhashi et al al. Journal of Laboratory Analysis. 1996. 10: 285-293.*
Lu et al. Clinical Cancer Research. 2004. 10: 3291-3300.*
Database Geneseq [Online] Dec. 2, 2004, Lilli I J. et al.: "Novel isolated polypeptide associated with breast cancer", XP002518625, retrieved from EBI, Database accession No. ACN90758.
Koslowski M et al: "Frequent nonrandom activation of germ-line genes in human cancer" Cancer Research, American Association for Cancer Research, Baltimore, MD, US, vol. 64, No. 17, Sep. 1, 2004, pp. 5988-5993, XP002309835, ISSN: 0008-5472.
Tuereci Ozlem et al: "Computational dissection of tissue contamination for identification of colon cancer-specific expression profiles." The FASEB Journal: Official Publication of the Federation of American Societies for Experimental Biology Mar. 2003, vol. 17, No. 3, Mar. 2003, pp. 376-385, XP002471061, ISSN: 1530-6860.
Prokopenko P. G et al: "Antigenic structure of ovarian cancer metastases." Bulletin of Experimental Biology and Medicine Jun. 2001, vol. 131, No. 6, Jun. 2001, pp. 561-563, XP002471062, ISSN: 0007-4888.
International Search Report for PCT/EP2008/008924, published Sep. 24, 2009, 6 pages.
International Preliminary Report on Patentability and Written Opinion of the International Searching Authority for PCT/EP2008/008924, 10 pages.
Harandi, "Immunoplacental therapy, a potential multi-epitope cancer vaccine", Medical Hypotheses 2006, vol. 66, 1182-1187.
Klamp et al., "Expression profiling of autoimmun regulator AIRE mRNA in a comprehensive set of human normal and neoplasitc tissues," Immunology Letters 2006, vol. 106, 172-179.
Koslowski et al., "A Placenta-specific gene ectopically activated in many human cancers is essentially involved in malignant cell processes," Cancer Research 2007, vol. 67, No. 19, 9528-9534, XP002471063.

(Continued)

Primary Examiner — Carla Myers

(74) *Attorney, Agent, or Firm* — McAndrews Held & Malloy, Ltd.

(57) **ABSTRACT**

The present technology relates to genetic products the expression of which is associated with cancer diseases. The present technology also relates to the therapy and diagnosis of diseases in which the genetic products are expressed or aberrantly expressed, in particular cancer diseases.

14 Claims, 28 Drawing Sheets

(56) **References Cited**

OTHER PUBLICATIONS

Human colon cancer antigen encoding cDNA Seq ID No: 1454, http://www.ebu.ac.uk/cgi-bin/epo/epofetch?AAH34372, dated Feb. 29, 2008, 2 pages, XP-002471064.

Shi et al., J. Histochem. Cytochem. 39: 741-748, 1991.

Shin et al., Lab. Invest. 64: 693-702, 1991.

Simpson AJ et al., Nat Rev Cancer 5: 615-25, 2005.

So et al., Mol. Cells 7: 178-186, 1997.

Spiller et al., J. Immunol. Methods 224: 51-60, 1999.

Stanislawski et al., Nat Immunol. 2: 962-70, 2001.

Stockton et al. 2001. Mol. Biol. Cell. 12: 1937-56.

Tuschl T. et al., "The siRNA User Guide", revised Oct. 11, 2002.

Zambrowicz BP & Sands AT. 2003. Nat. Rev. Drug Discov. Jan. 2003; 2(1): 38-51.

Ito Hirotaka et al: "Identification of ROBO1 as a novel heptacellular carcinoma antigen and a potential therapeutic and diagnostic target", Clinical Cancer Research: An Official Journal of the American Association for Cancer Research, vol. 12, No. 11 Pt 1, Jun. 1, 2006, pp. 3257-3264.

Database Geneseq [Online], May 5, 2005, Aburatani H et al: "Human TEG6 associated DNA Seq", Database accession No. ADX83391.

Xie M-H et al: "FGF-19, A Novel Fibroblast Growth Factor With Unique Specificity for FGFR4", Cytokine, Academic Press Ltd, Phiadelphia, PA, US, vol. 11, No. 10, Oct. 1, 1999, pp. 729-735.

Goddard A et al: "Human Pro Protein #33", 1-7 Genbank, Jan. 1, 2004.

Database UniProt [Online], May 20, 2004, Isogai T. et al.: "New polynucleotides and polypeptides useful in gene therapy, ...", retrieved from EBI, Database accession No. ADM02094.

Abate-Shen & Shen. 2002. Trends in Genetics S1-5.

Acevedo HF et al., Cancer 76: 1467-75, 1995.

Adams GP, Weiner LM, Nat Biotechnol 23: 1147-57, 2005.

Altman et al., Science 274: 94-96, 1996.

Anderson et al., J. Immunol. 143: 1899-1904, 1989.

Azorsa et al., J. Immunol. Methods 229: 35-48, 1999.

Balling R, 2001. Ann. Rev. Genomics Hum. Genet. 2: 463-92.

Beard J, Lancet 1: 1758-63, 1902.

Chomczynski & Sacchi, Anal. Biochem. 162: 156-159, 1987.

Cinamon G., Alon R. J. Immunol. Methods. Feb. 2003; 273(1-2): 53-62.

Clark, W.R. (1986), The Experimental Foundations of Modern Immunology, Wiley & Sons, Inc., New York.

Czauderna et al. 2003. Nucl. Acid Res. 31: 670.82.

de Wildt et al., J. Immunol. Methods 207: 61-67, 1997.

Dirnhofer S et al., Hum Pathol 29: 377-82, 1998.

Dunbar et al., Curr. Biol. 8: 413-416, 1998.

Durand & Seta, 2000; Clin. Chem. 46: 795-805.

Gardsvoll, J. Immunol. Methods 234: 107-116, 2000.

Goodman and Gilman, "The Pharmacological Basis of Therapeutics", 8th Edition, 1990, McGraw-Hill, Inc., in particular Chapter 52 (Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner).

Greenberg, J. Immunol. 136(5): 1917, 1986.

Gurchot C, Oncology 31: 310-3, 1975.

Hakomori, 1996; Cancer Res. 56: 5309-18.

Hannon, GJ. 2002. RNA interference. Nature 418: 244.51.

Iles RK, Chard T, J Urol 145: 453-8, 1991.

Jegstrup I. et al. 2003. Lab Anim. Jan. 2003; 37(1): 1.9.

Jung et al., Mol. Cells 12: 41.49, 2001.

Kasinrerk et al., Hybrid Hybridomics 21: 287-293, 2002.

Kast et al., Cell 59: 603-614, 1989.

Kayyem et al., Eur. J. Biochem. 208: 1-8, 1992.

Kessels et al., Nat Immunol. 2: 957-61, 2001.

Koslowski, M. et al., Cancer Res. 62, 6750-6755 (2002).

Kreig et al., Nature 374: 546-9, 1995.

Laurence DJ, Neville AM, Br J Cancer 26: 335-55, 1972.

Lemoine et al., Methods Mol. Biol. 75: 441-7, 1997.

Lynch et al., Eur. J. Immunol. 21: 1403-1410, 1991.

Maloy et al., Proc Natl Acad Sci USA 98: 3299-303, 2001.

Matsusue et al. 2003. J. Clin. Invest. 111: 737-47.

Niwa H. 2001. Cell Struct. Funct. Jun. 2001; 26(3): 137-48.

Ossendorp et al., Immunol Lett. 74: 75-9, 2000.

Ossendorp et al., J. Exp. Med. 187: 693-702, 1998.

Pardoll, Nat. Med. 4: 525-31, 1998.

Peters T. et al. 2003. Hum. Mol. Genet 12: 2109-20.

Riddel et al., Science 257: 238, 1992.

Roitt, I. (1991), Essential Immunology, 7th Edition, Blackwell Scientific Publications, Oxford.
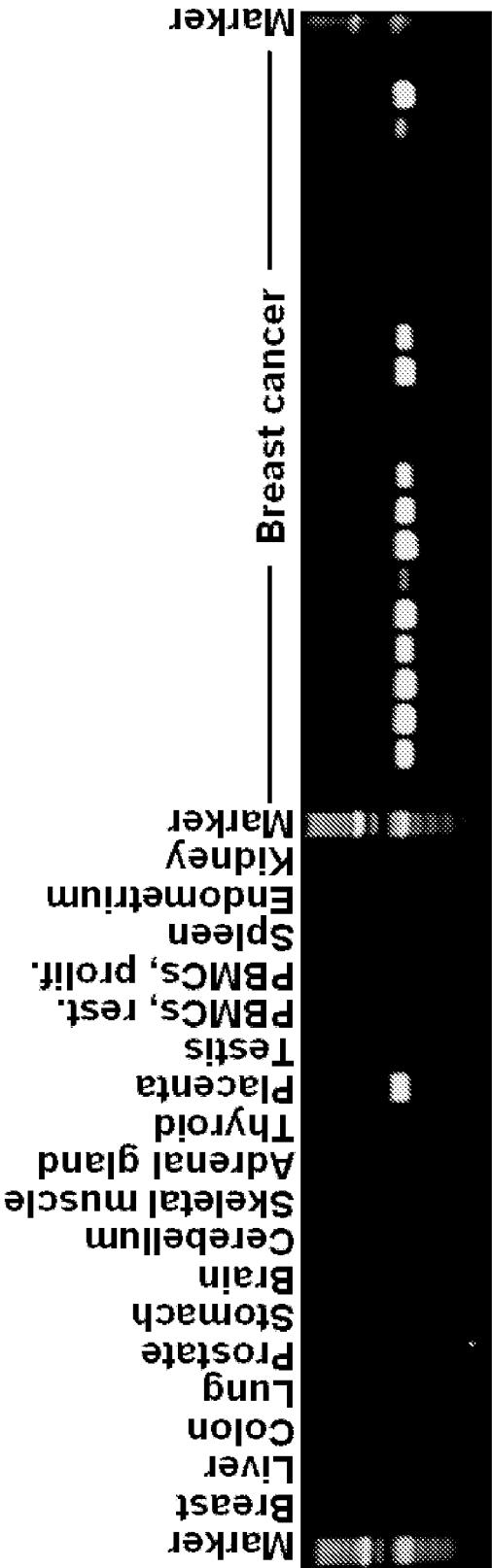
Sambrook, J. et al., "Molecular Cloning: A Laboratory Manual", Editors, 2nd Edition, Cold Spring Harbor Laboratory press, Cold Spring Harbor, New York, 1989.

Science 268: 1432-1434, 1995.

* cited by examiner

Fig. 1

Fig. 2

Fig. 3

Fig. 4

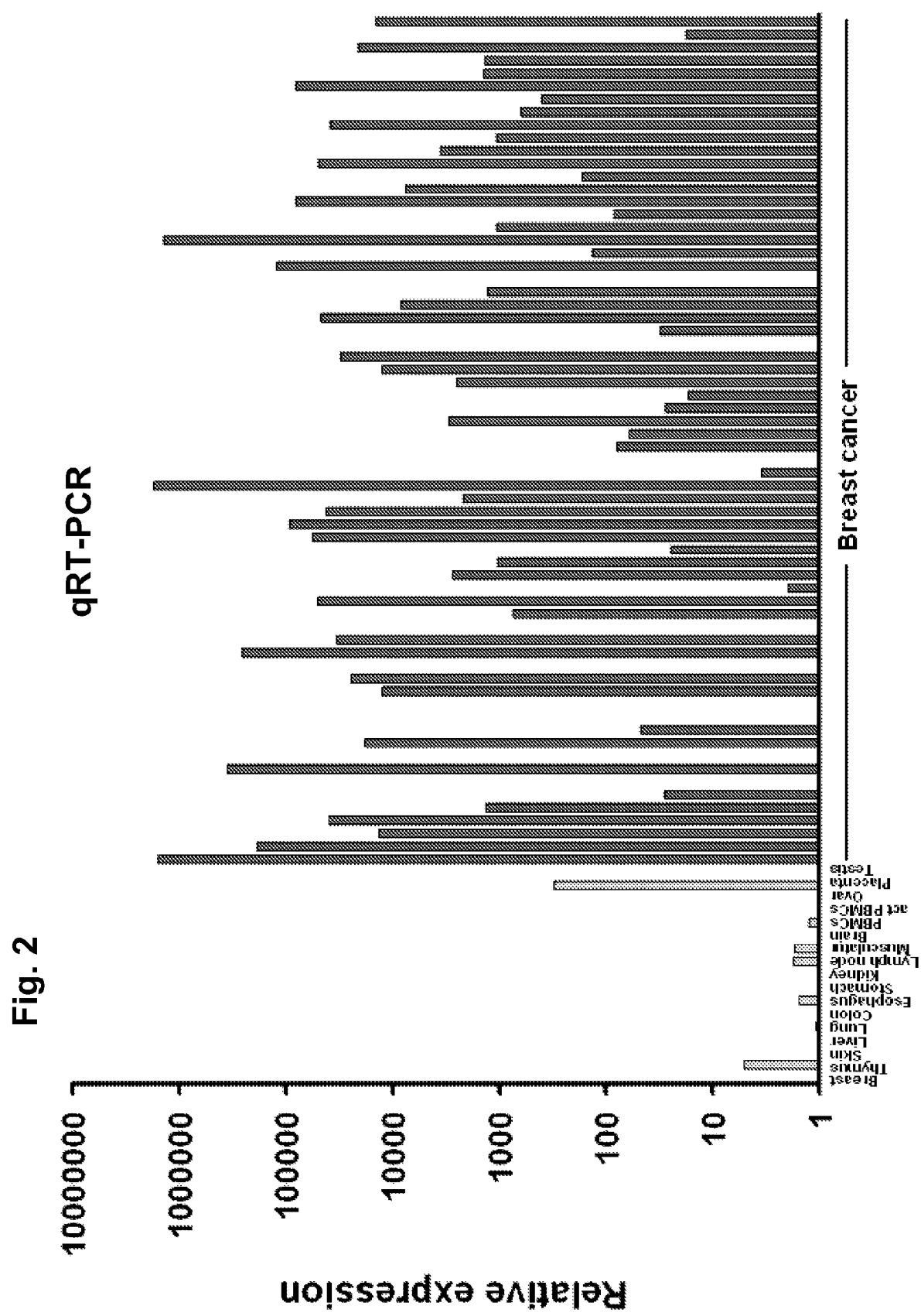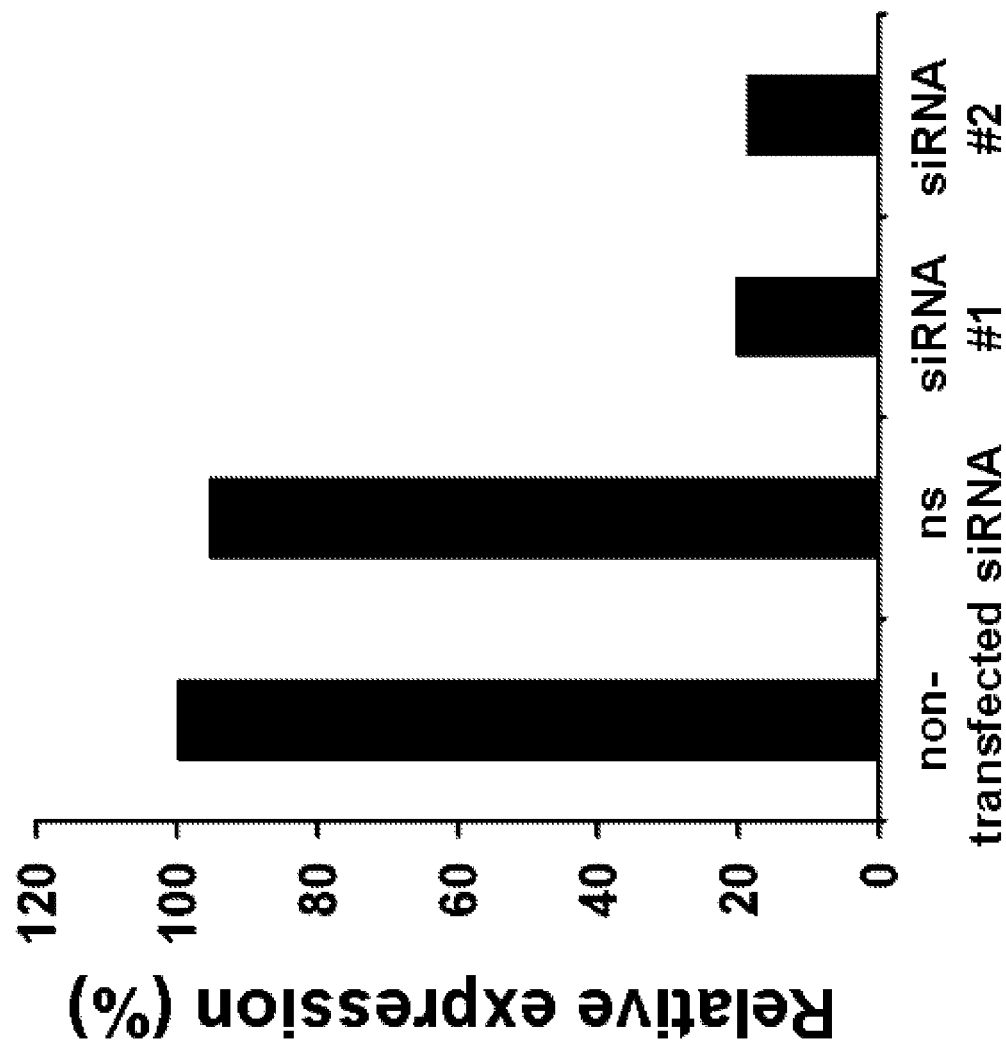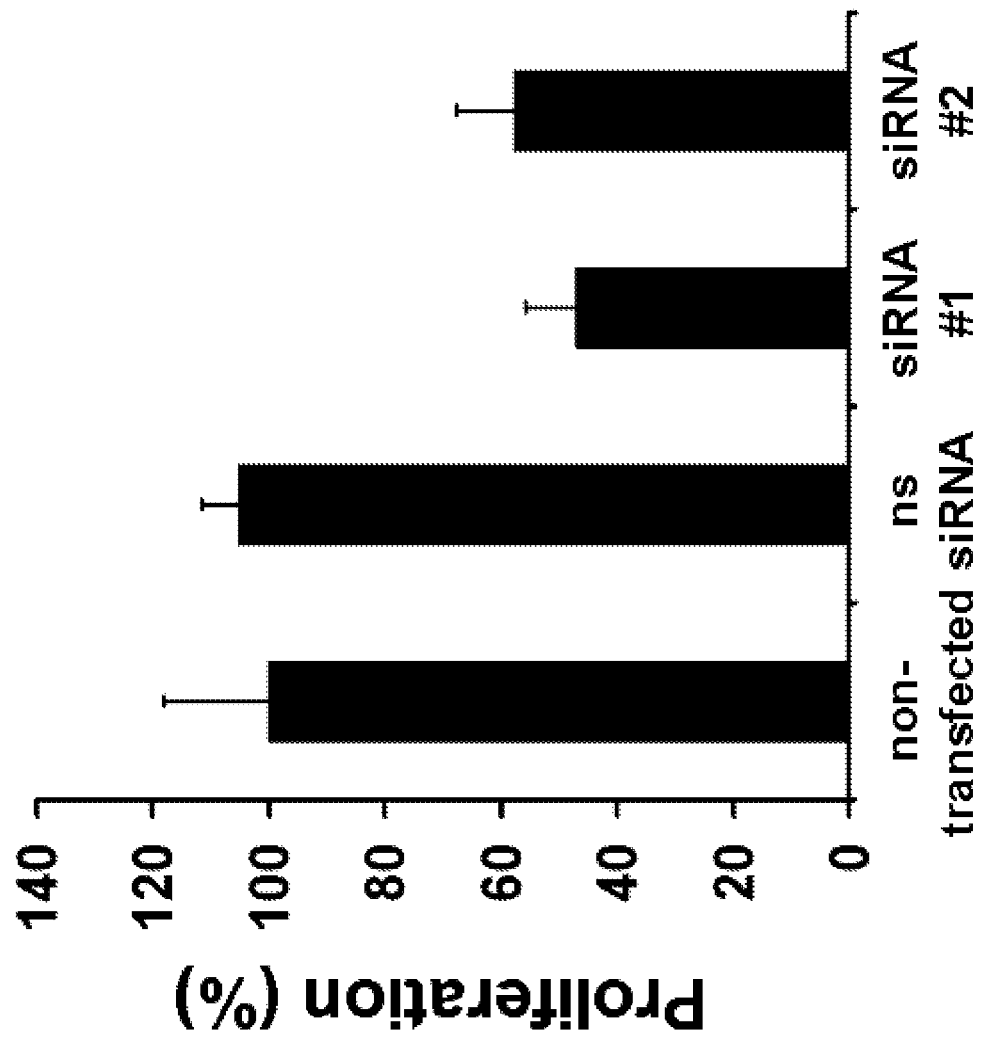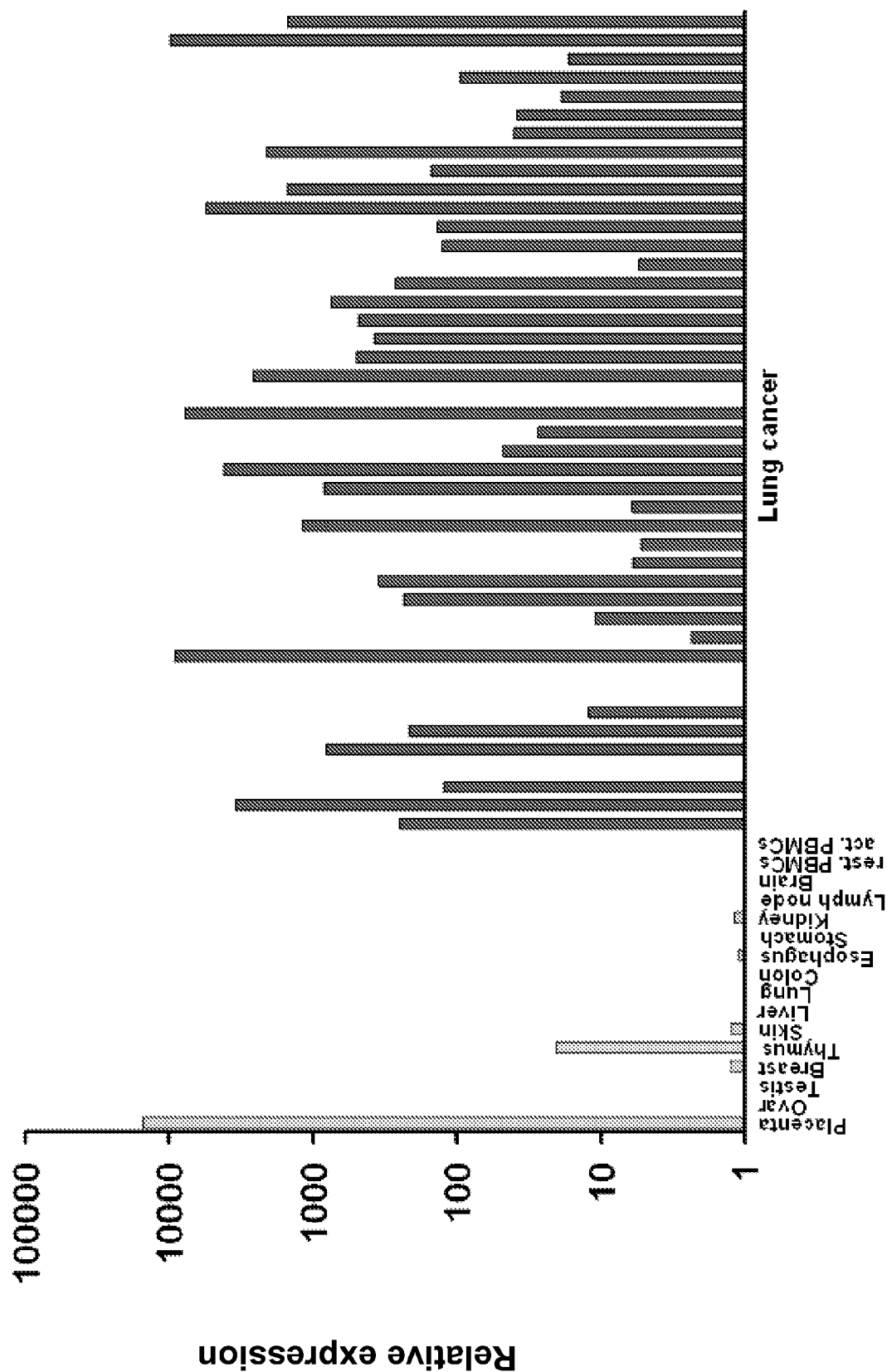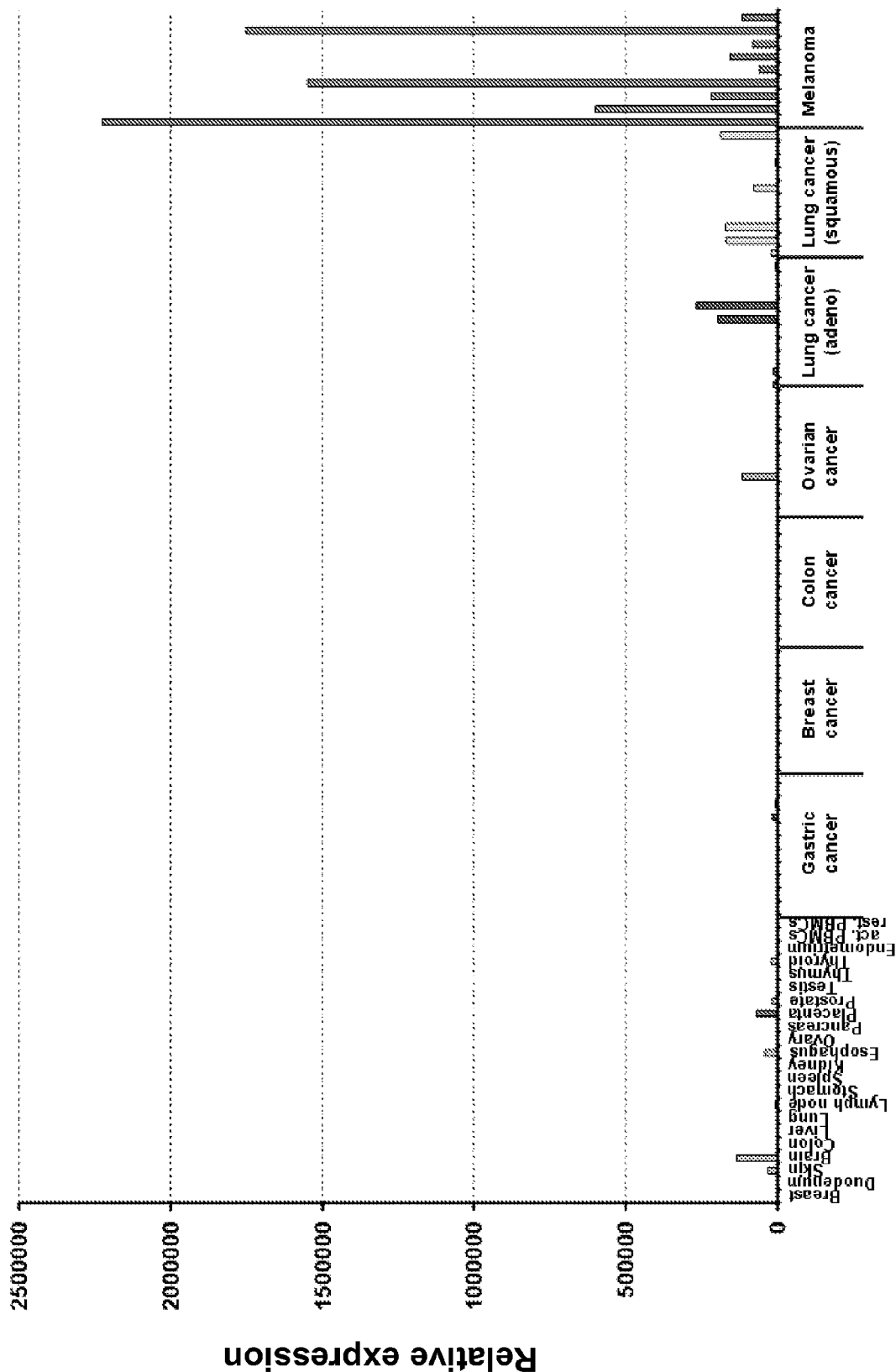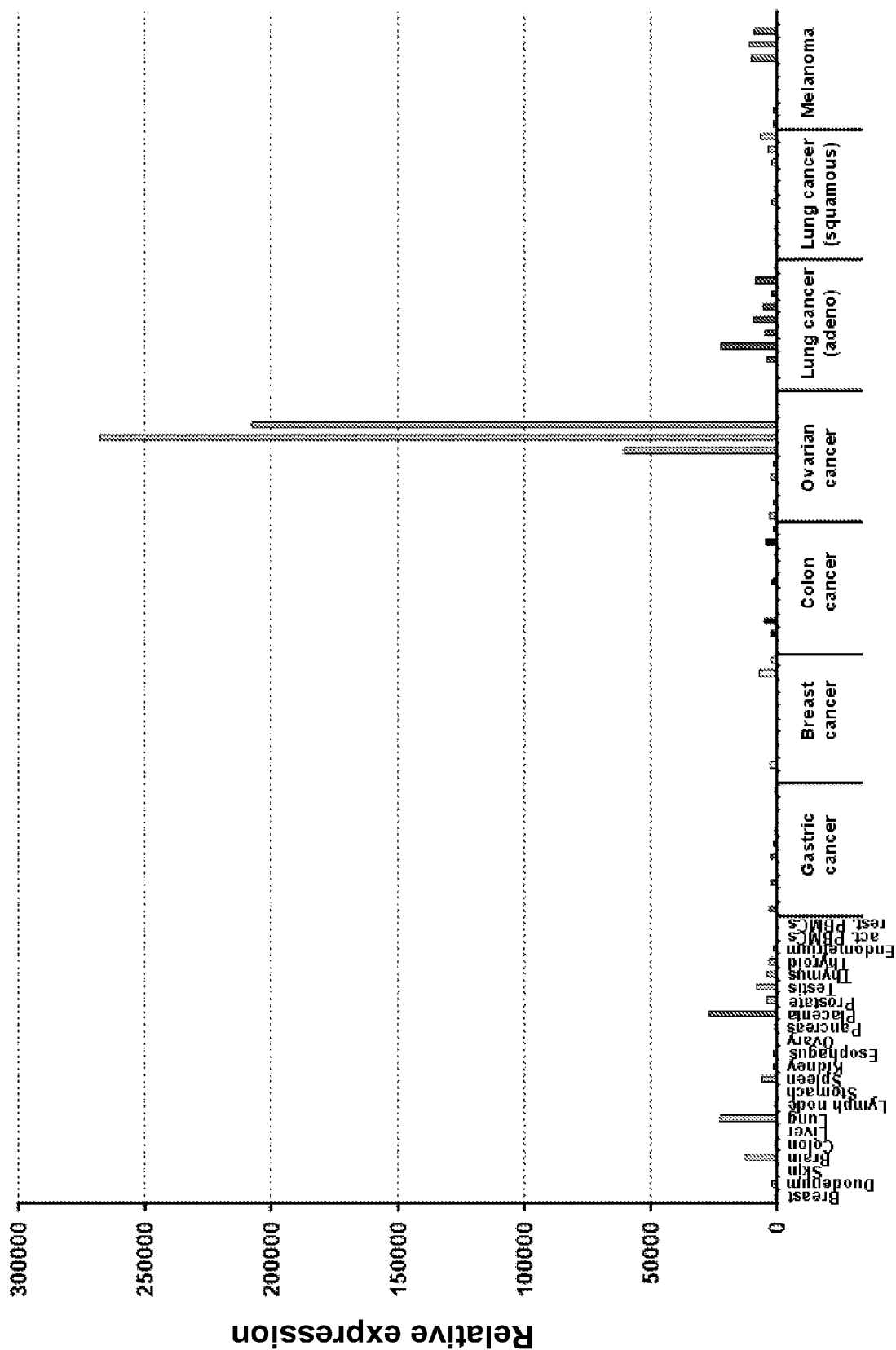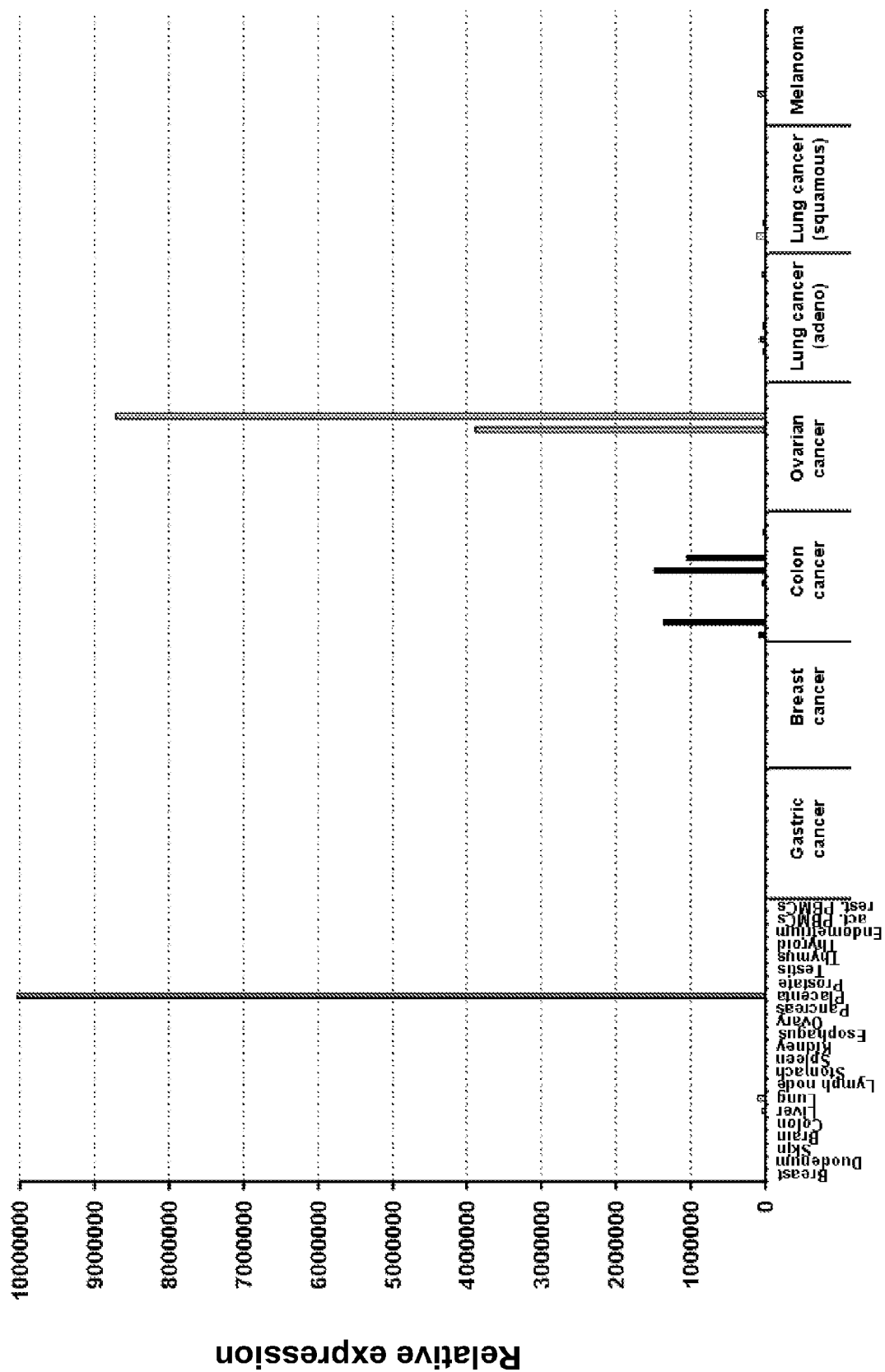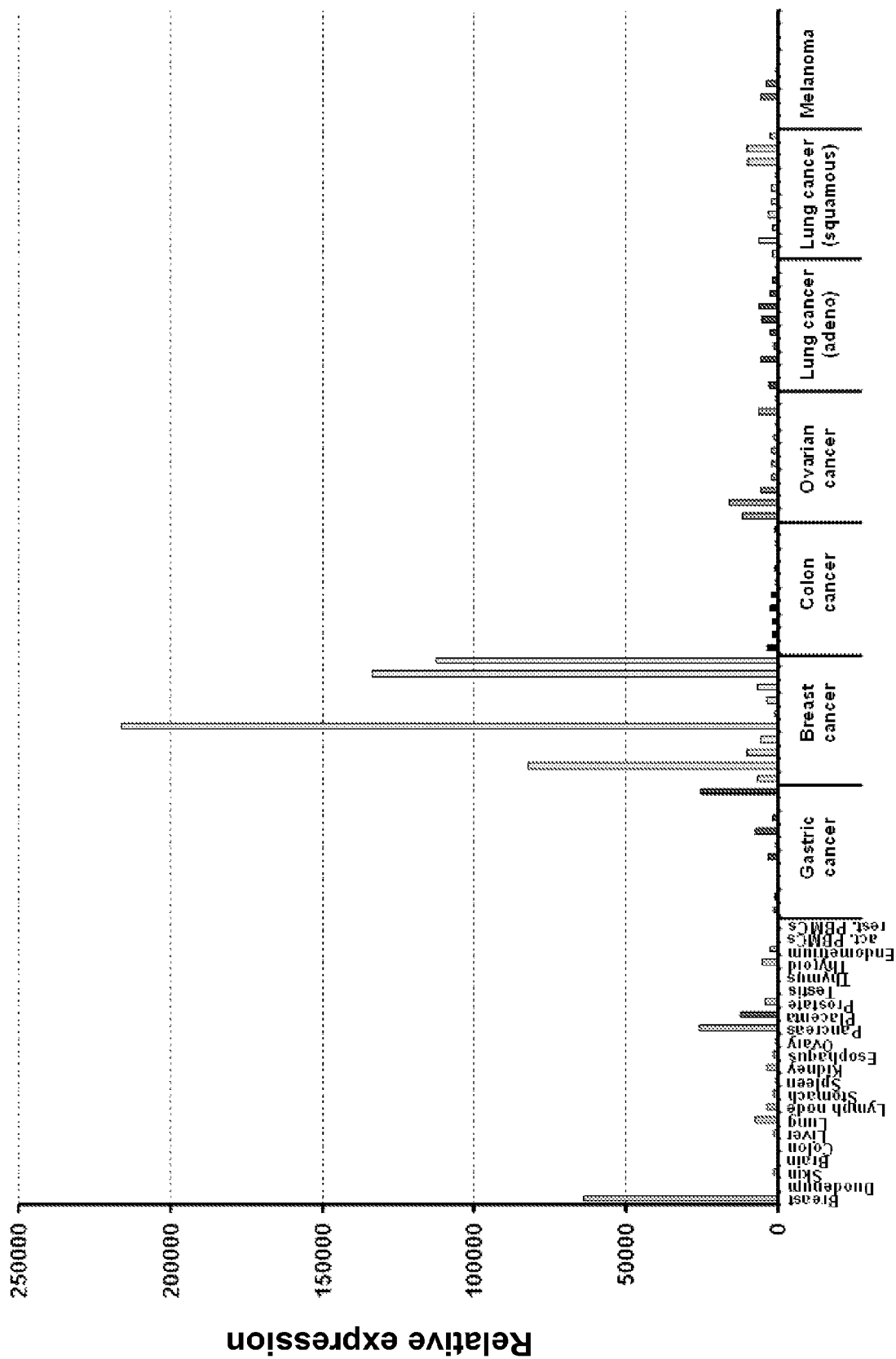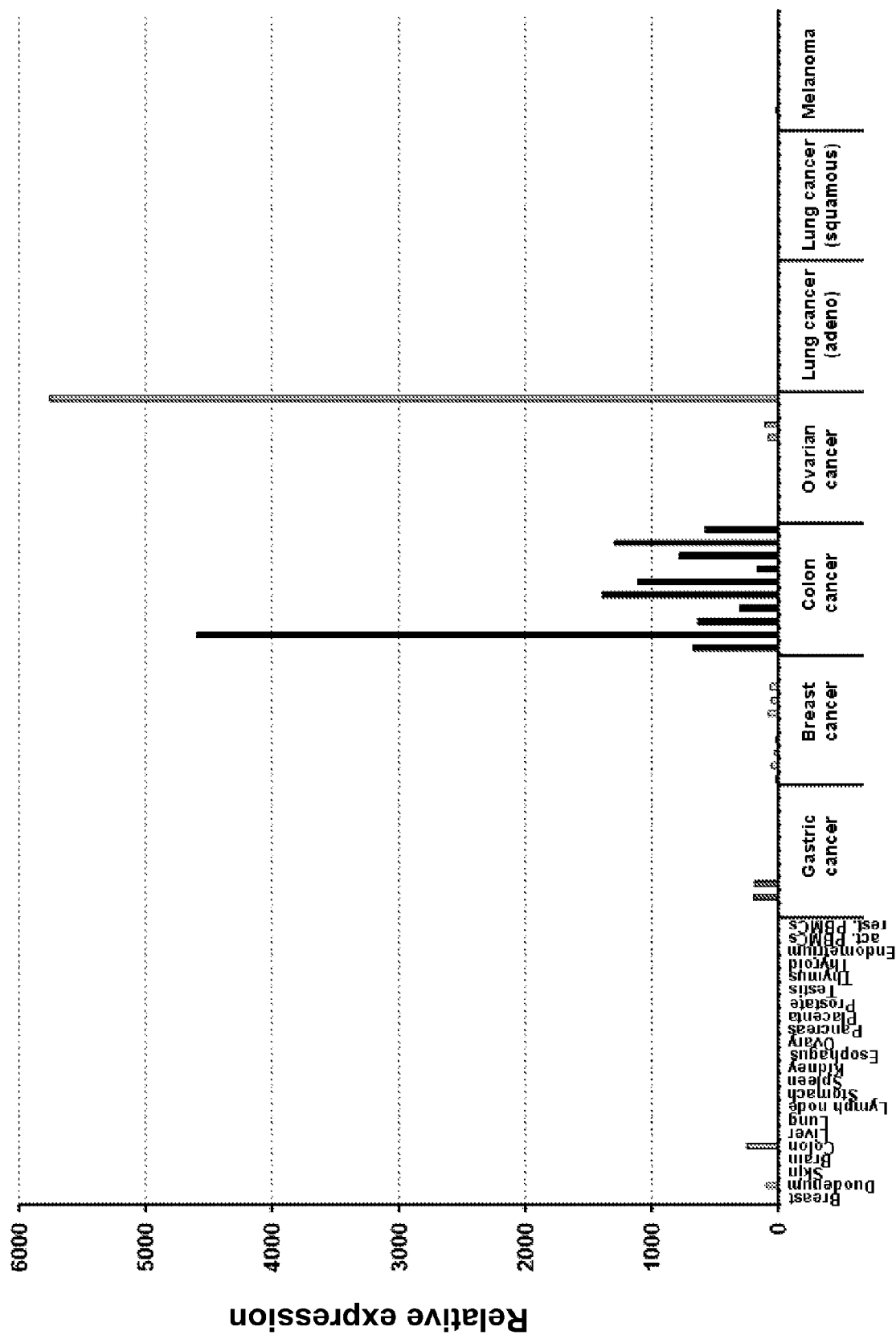Fig. 5

Fig. 6

Fig. 7

Fig. 8

Fig. 9

Fig. 10

Fig. 11
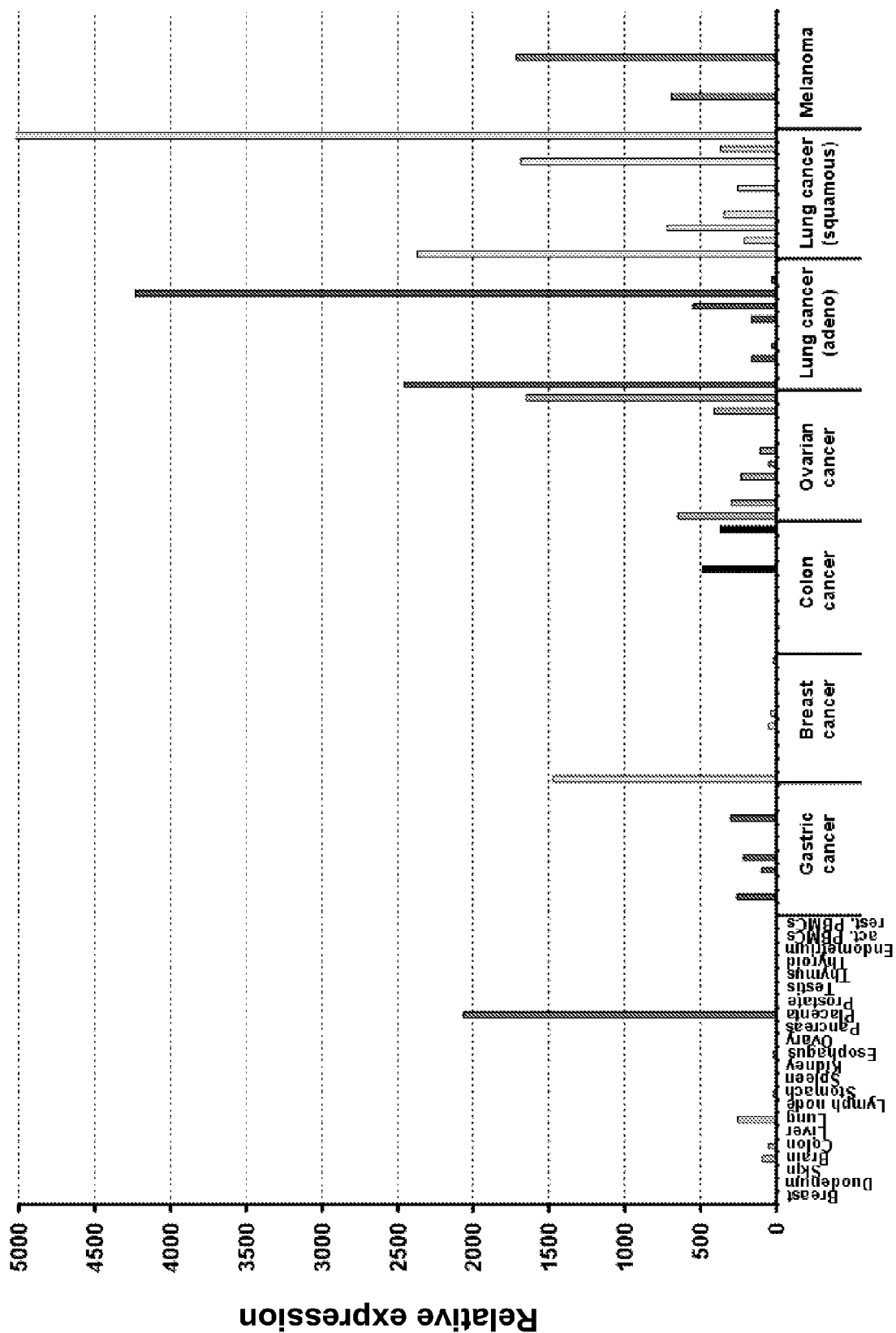
Fig. 12

Fig. 13

Fig. 14
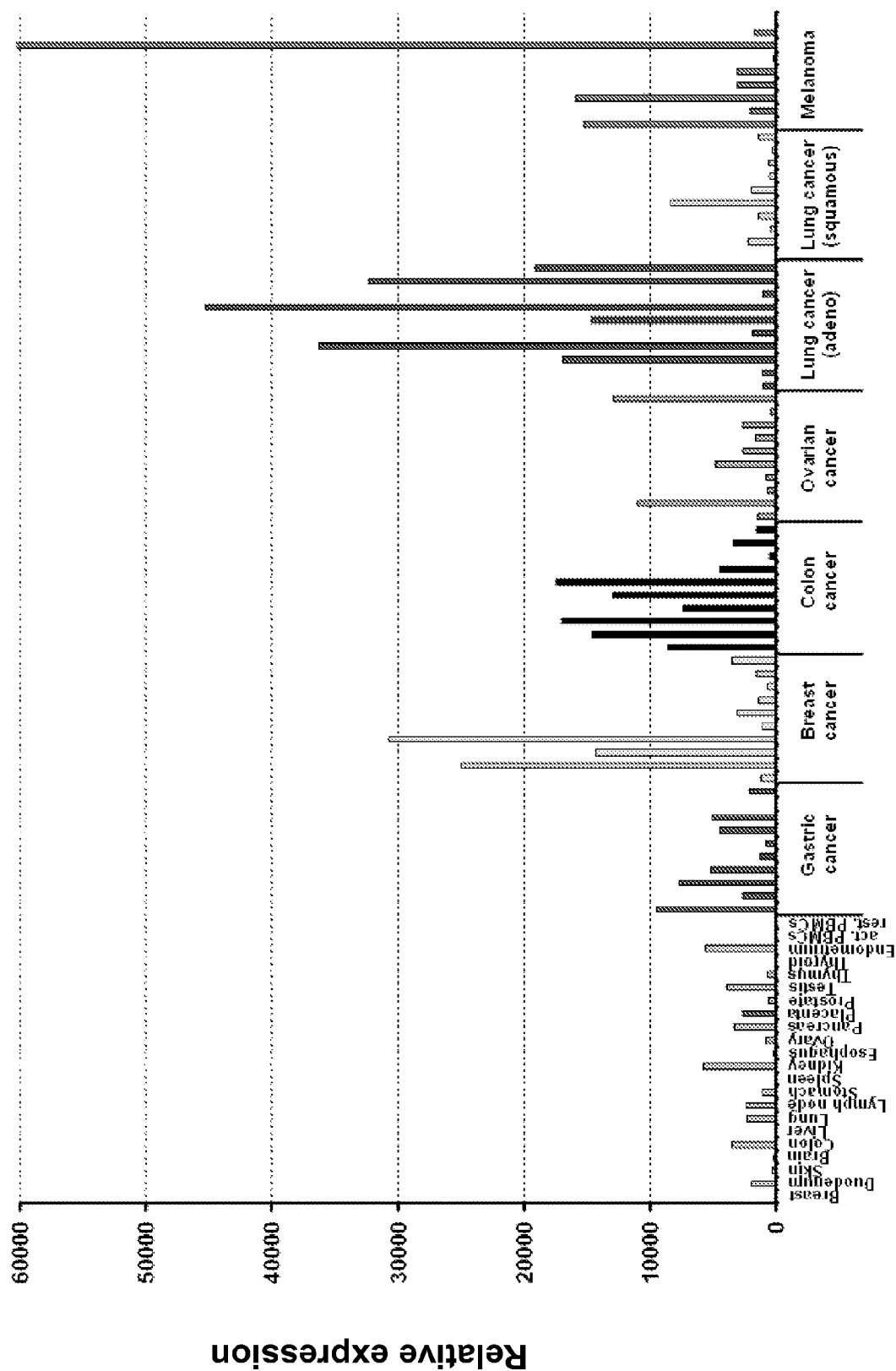
Fig. 15

Fig. 16

Fig. 17
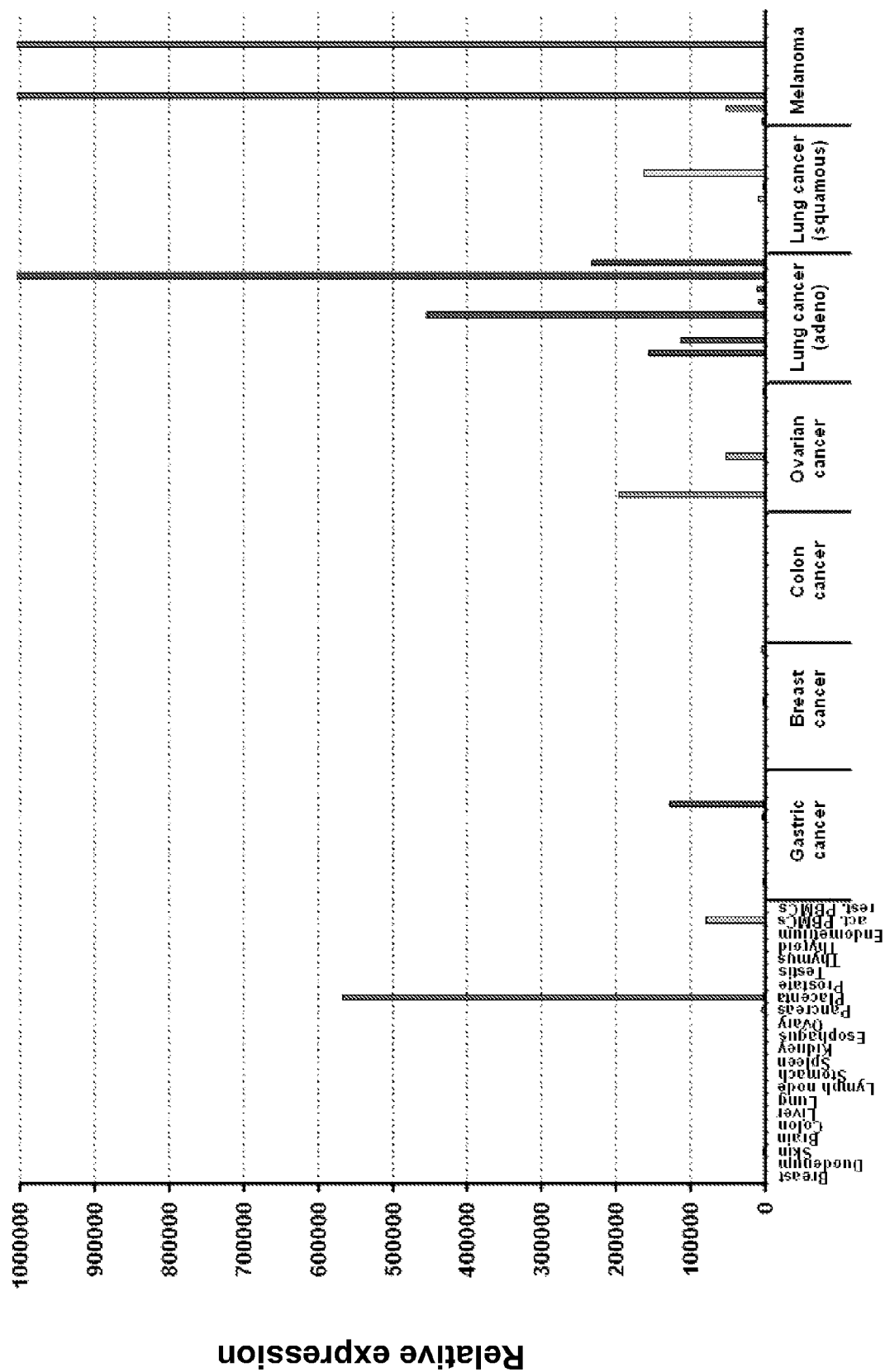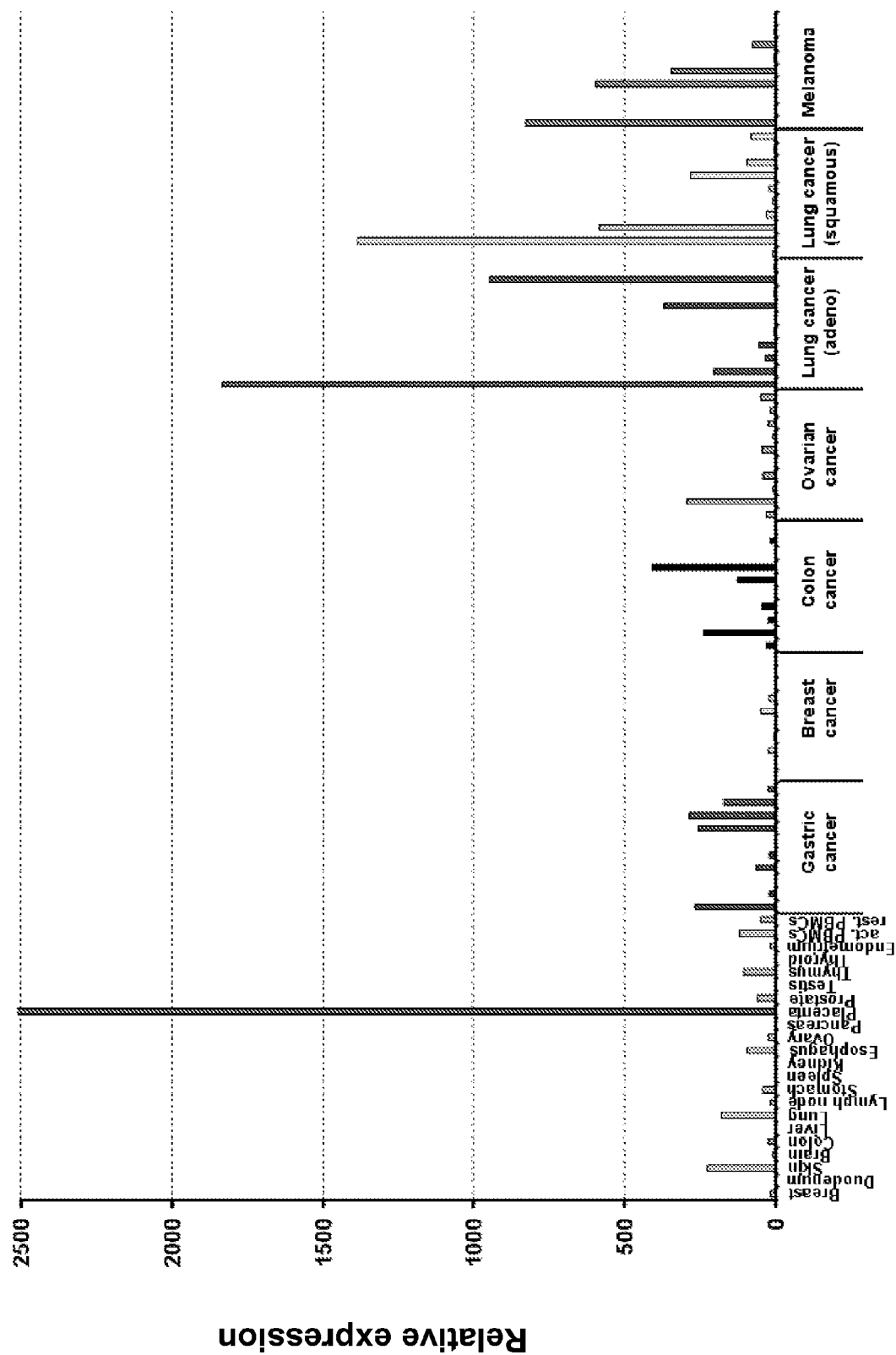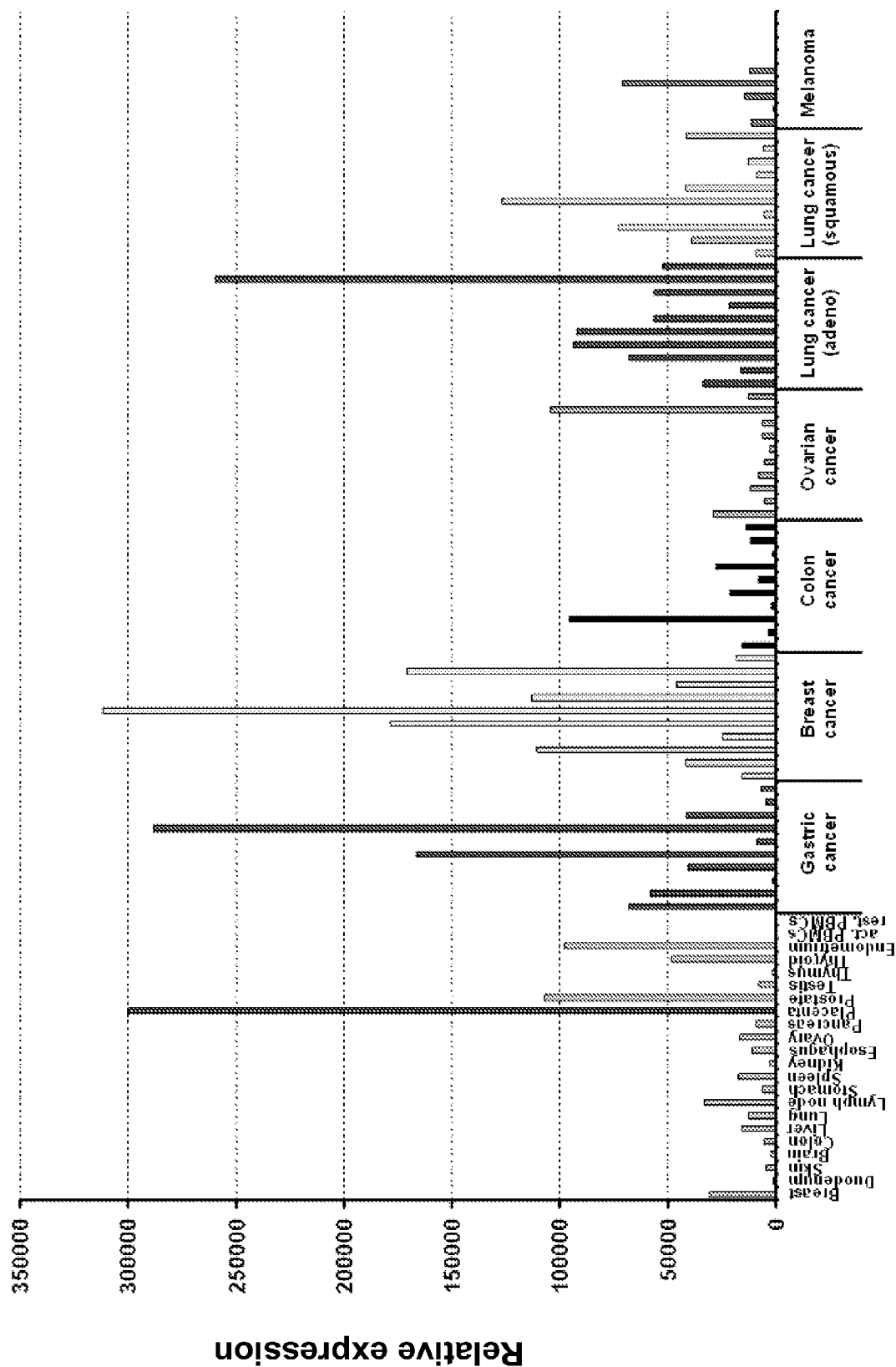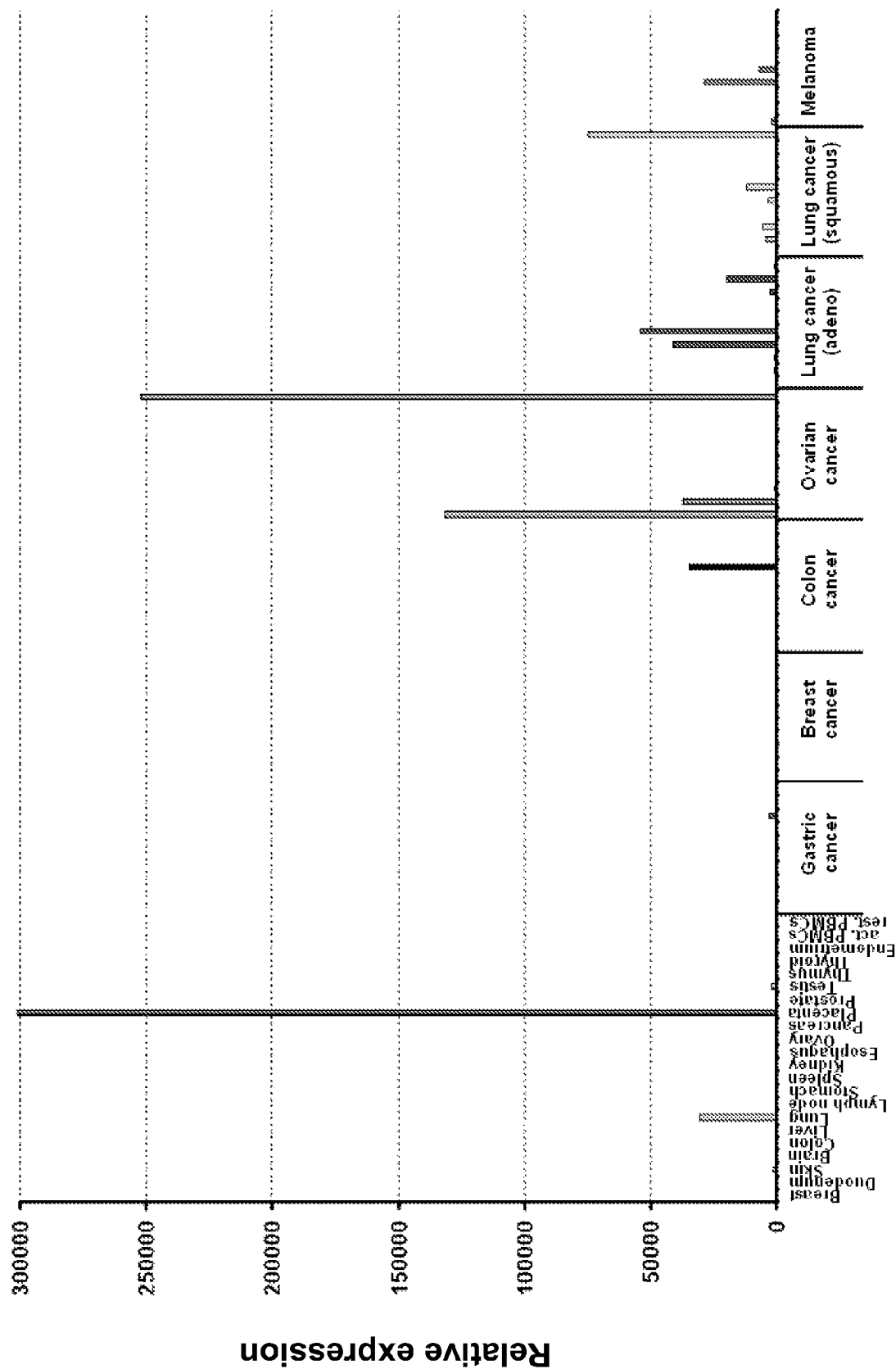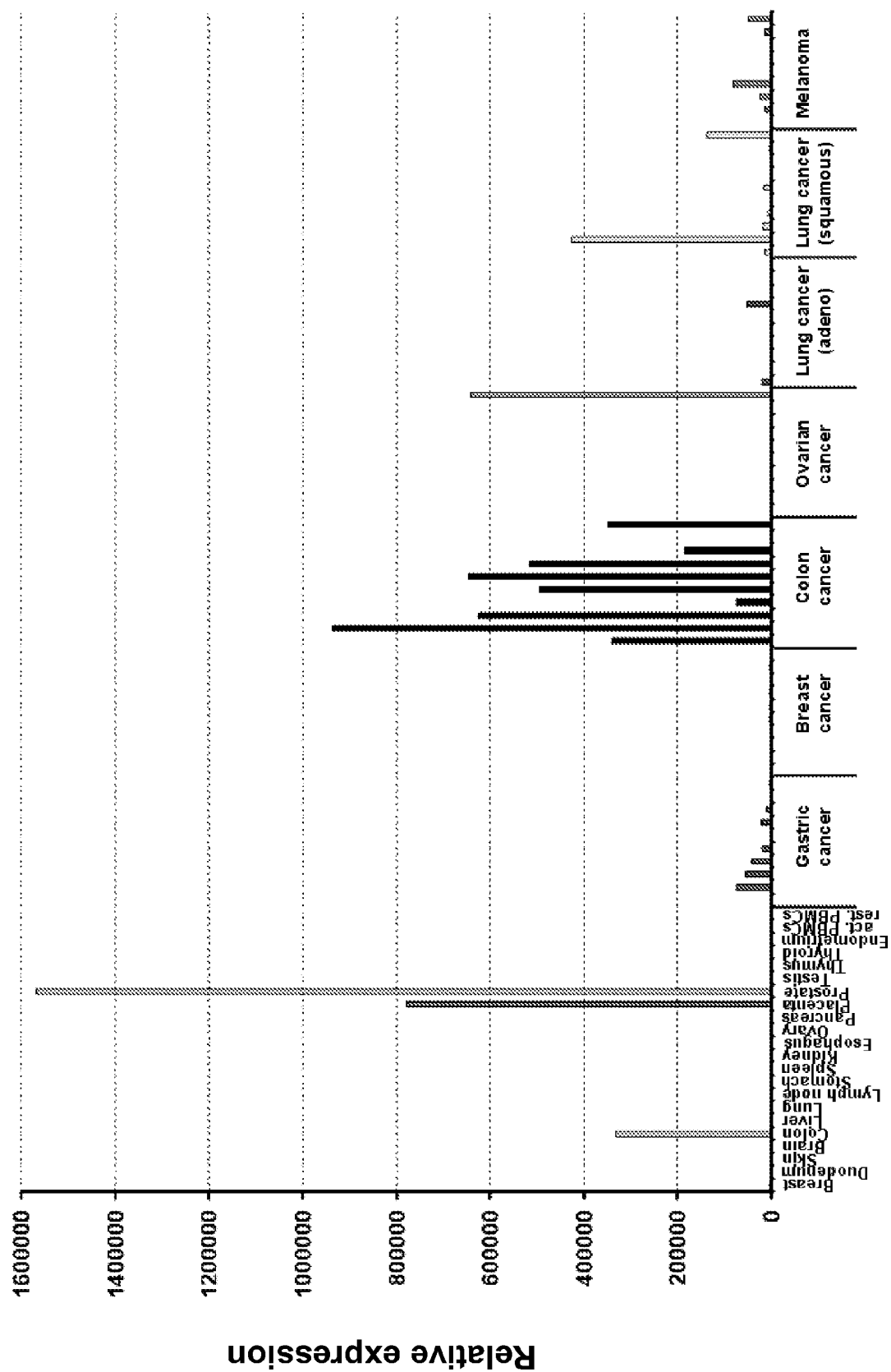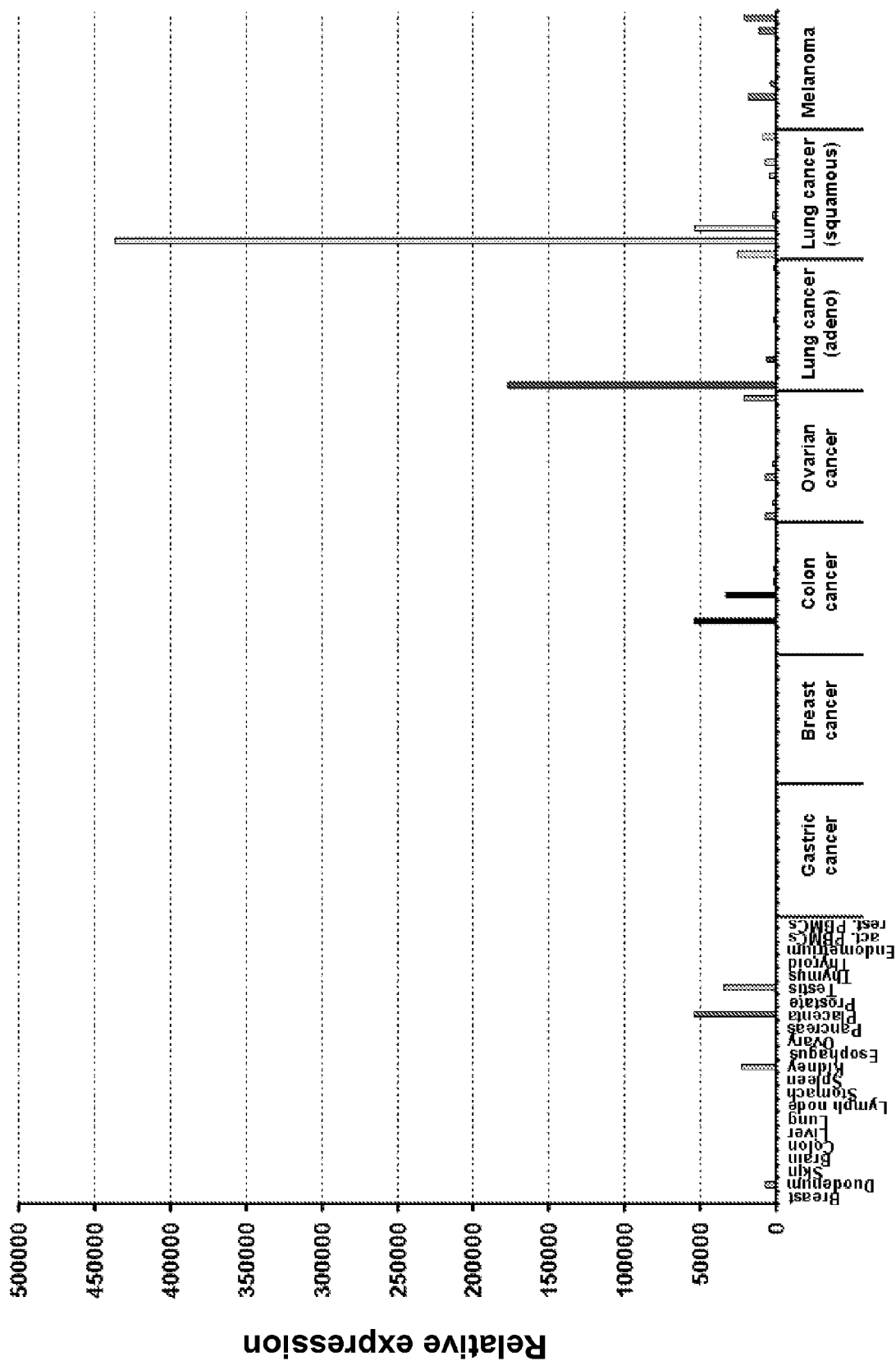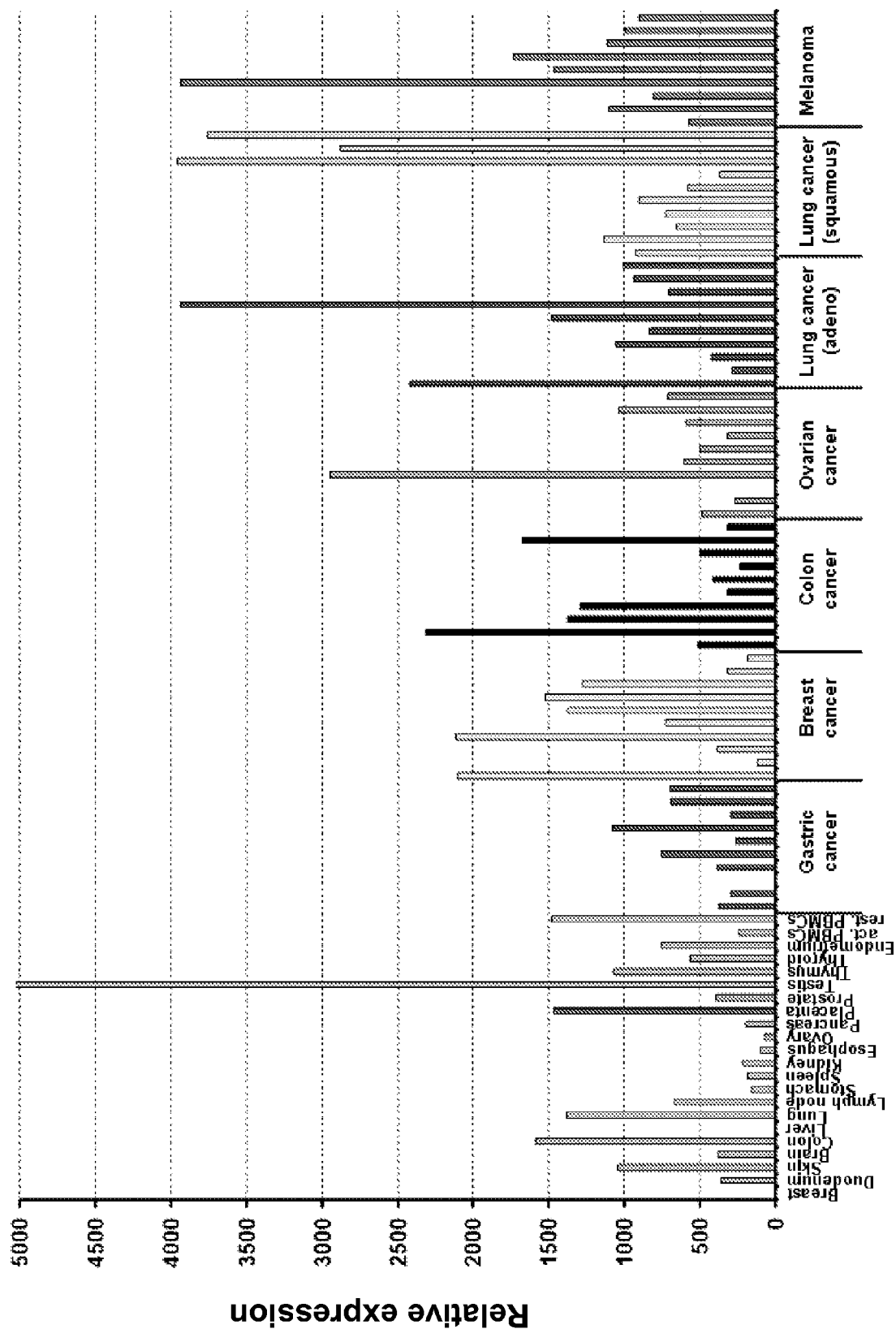
Fig. 18

Fig. 19

Fig. 20

Fig. 21

Fig. 22

Relative expression
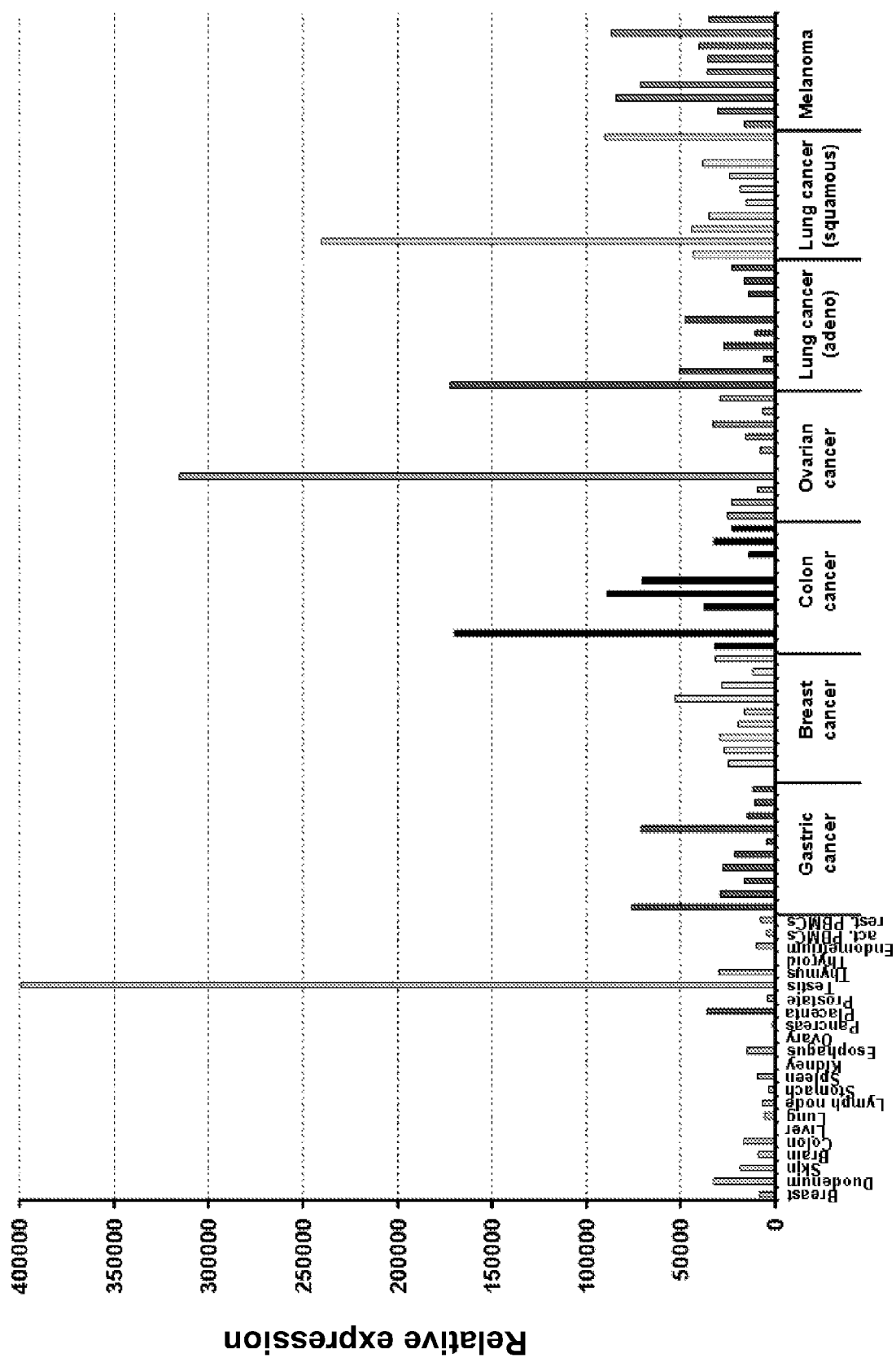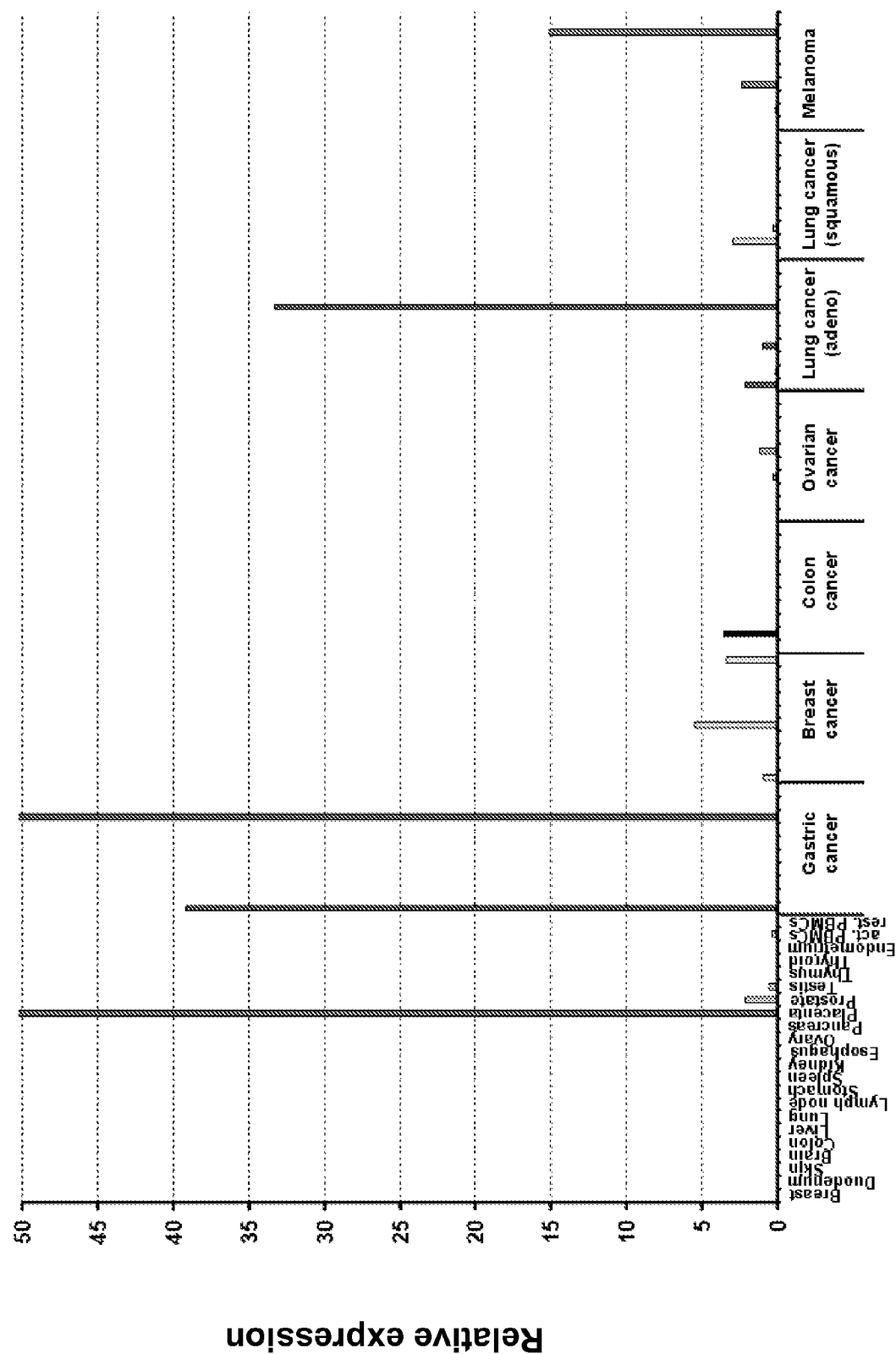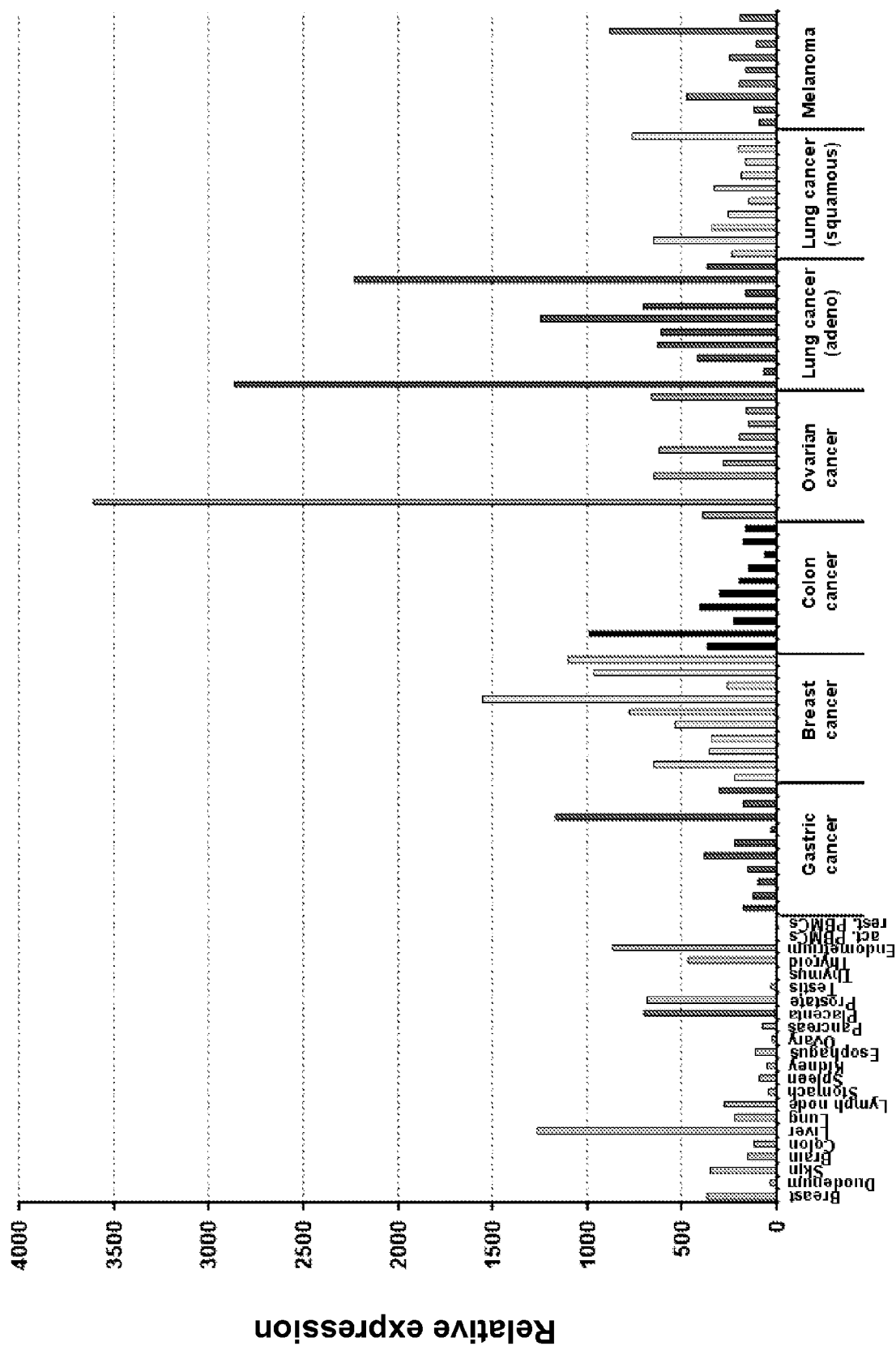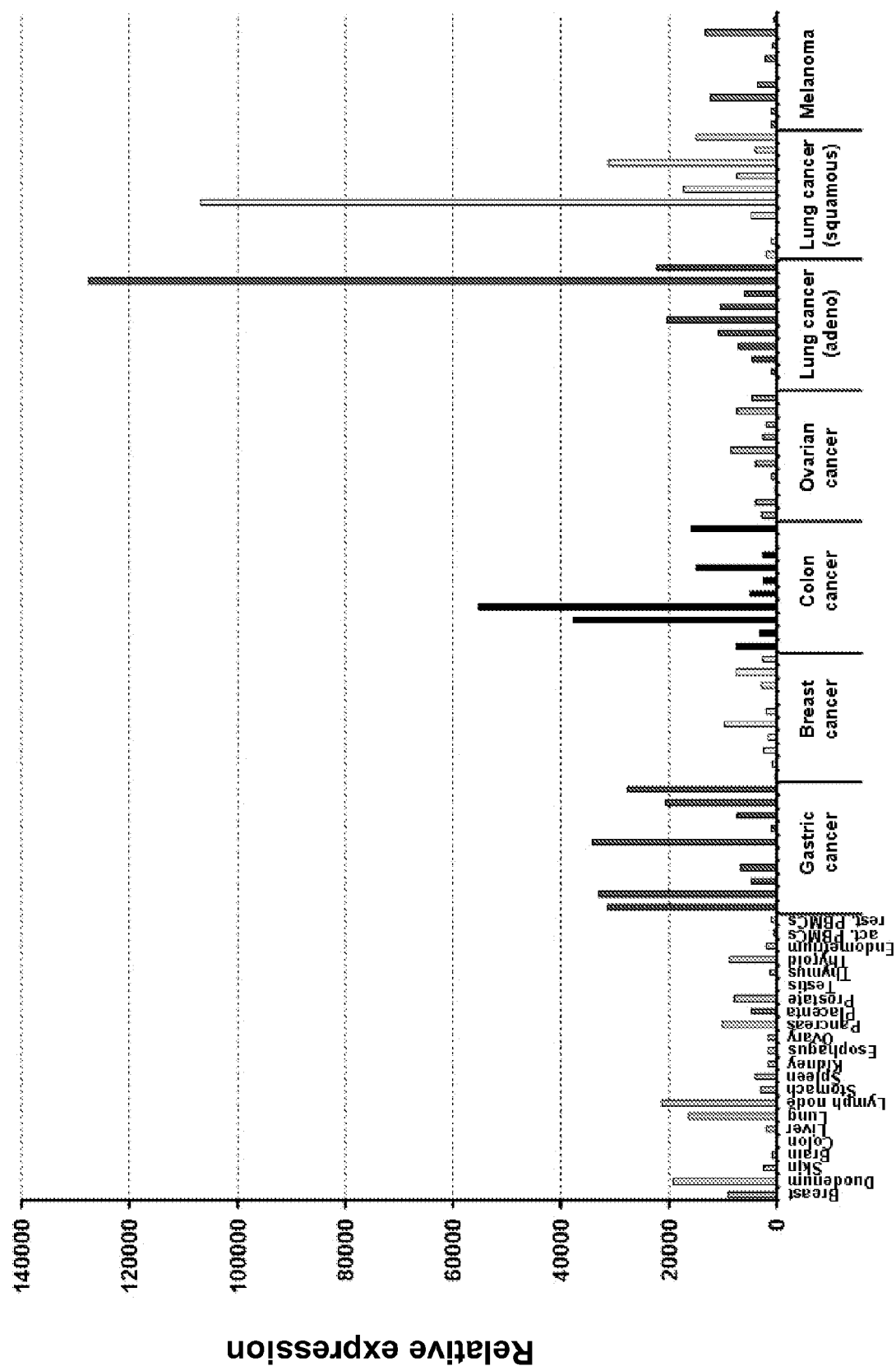
Fig. 23

Fig. 24
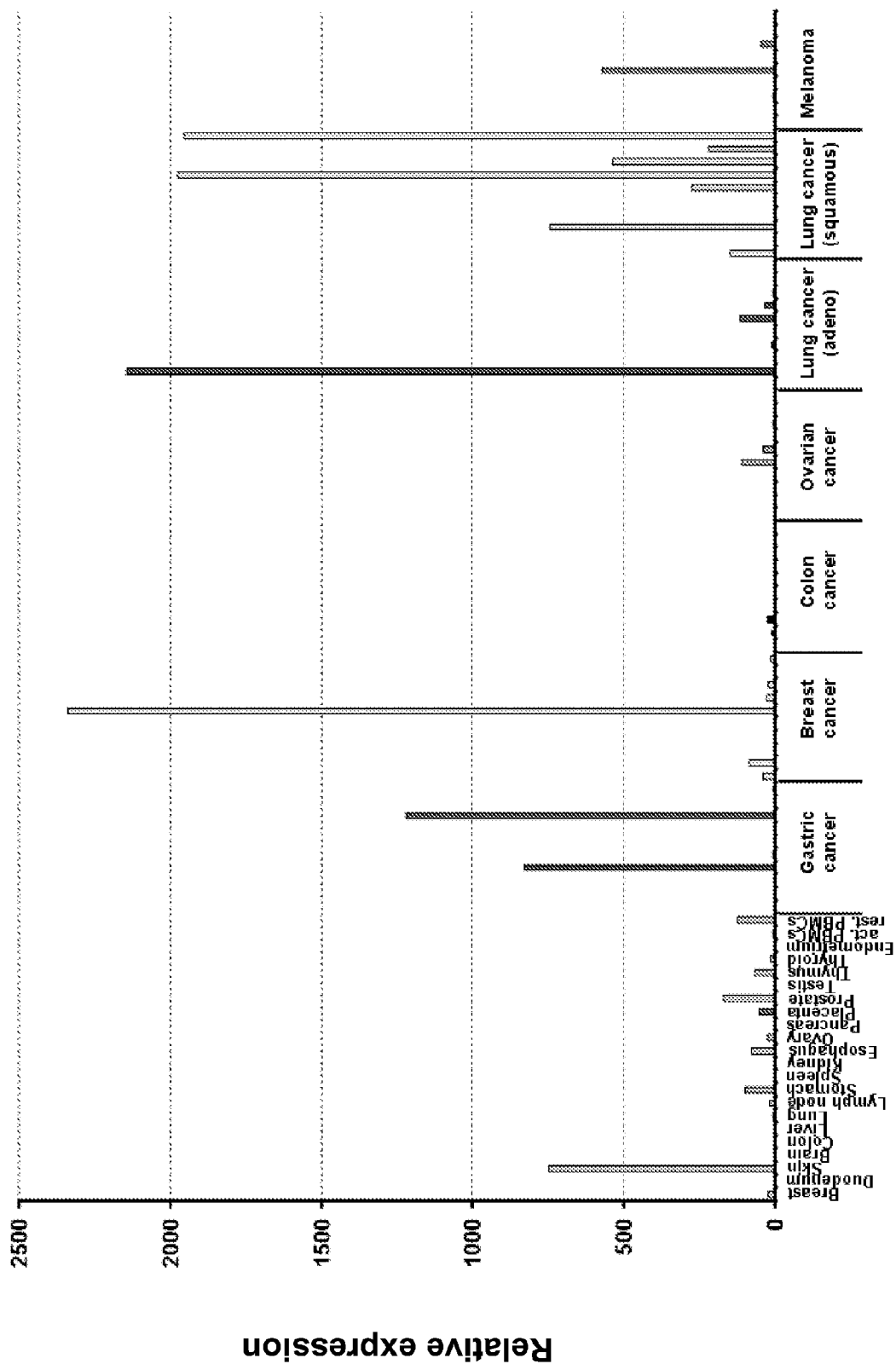
Fig. 25

Fig. 26
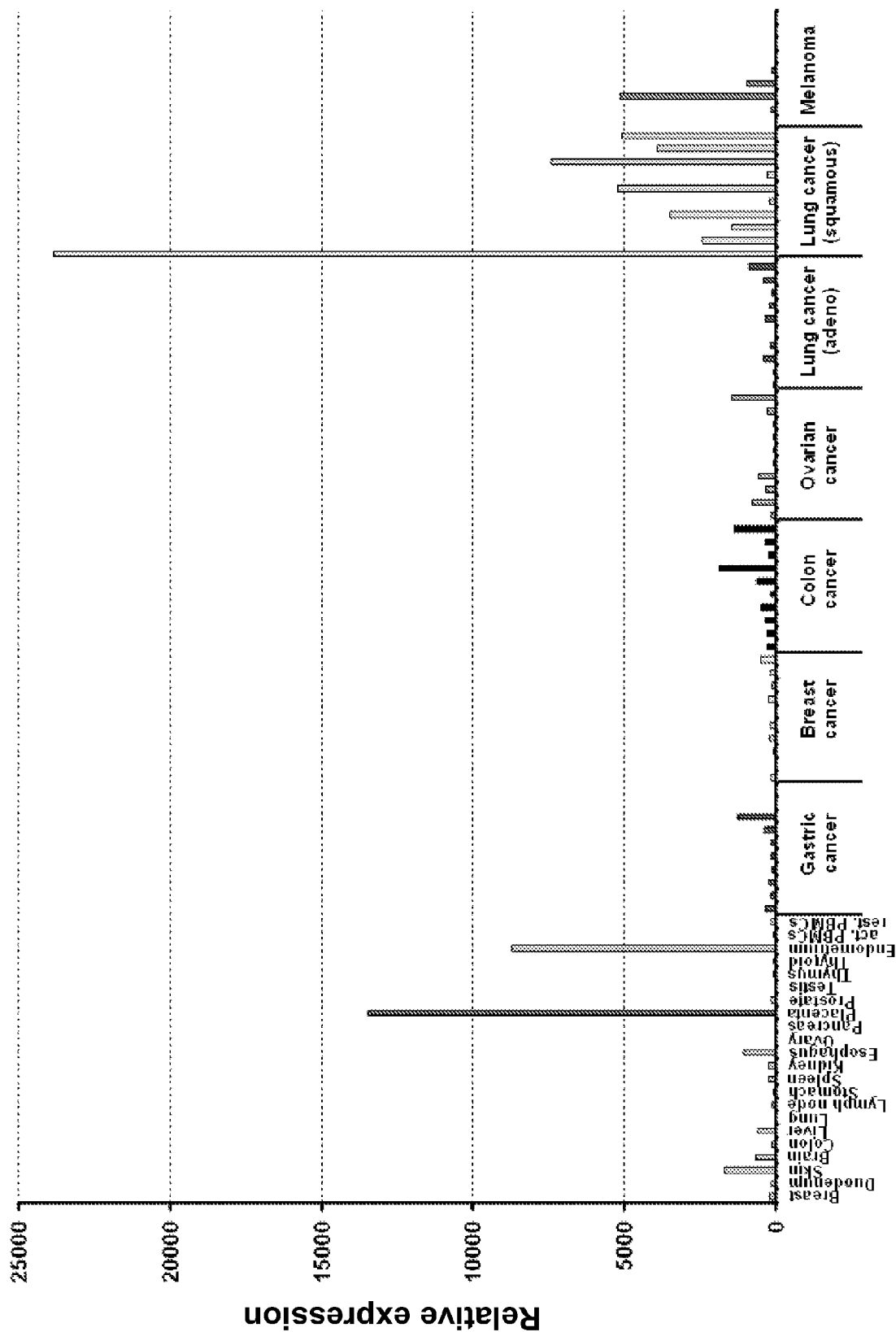
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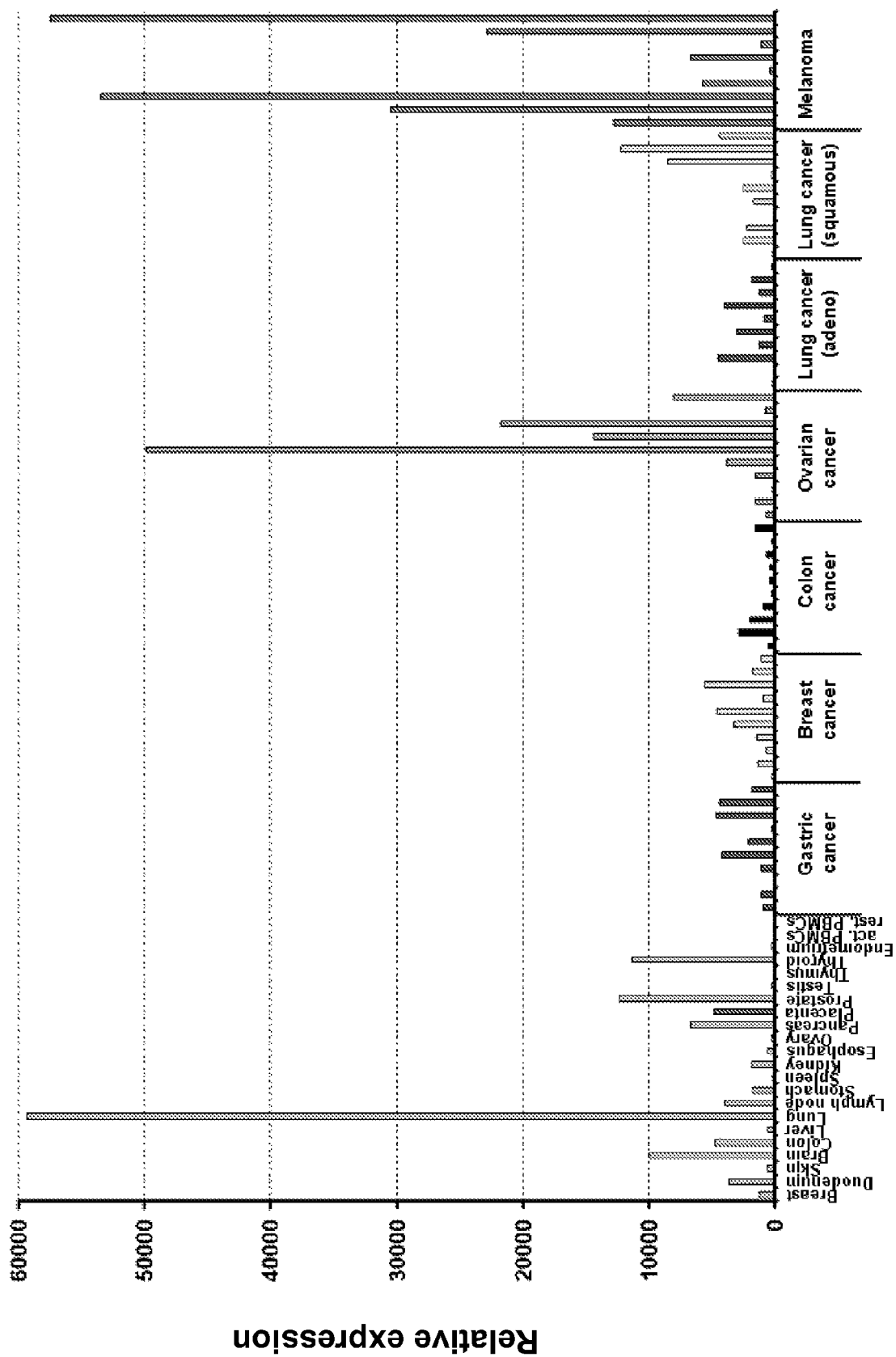
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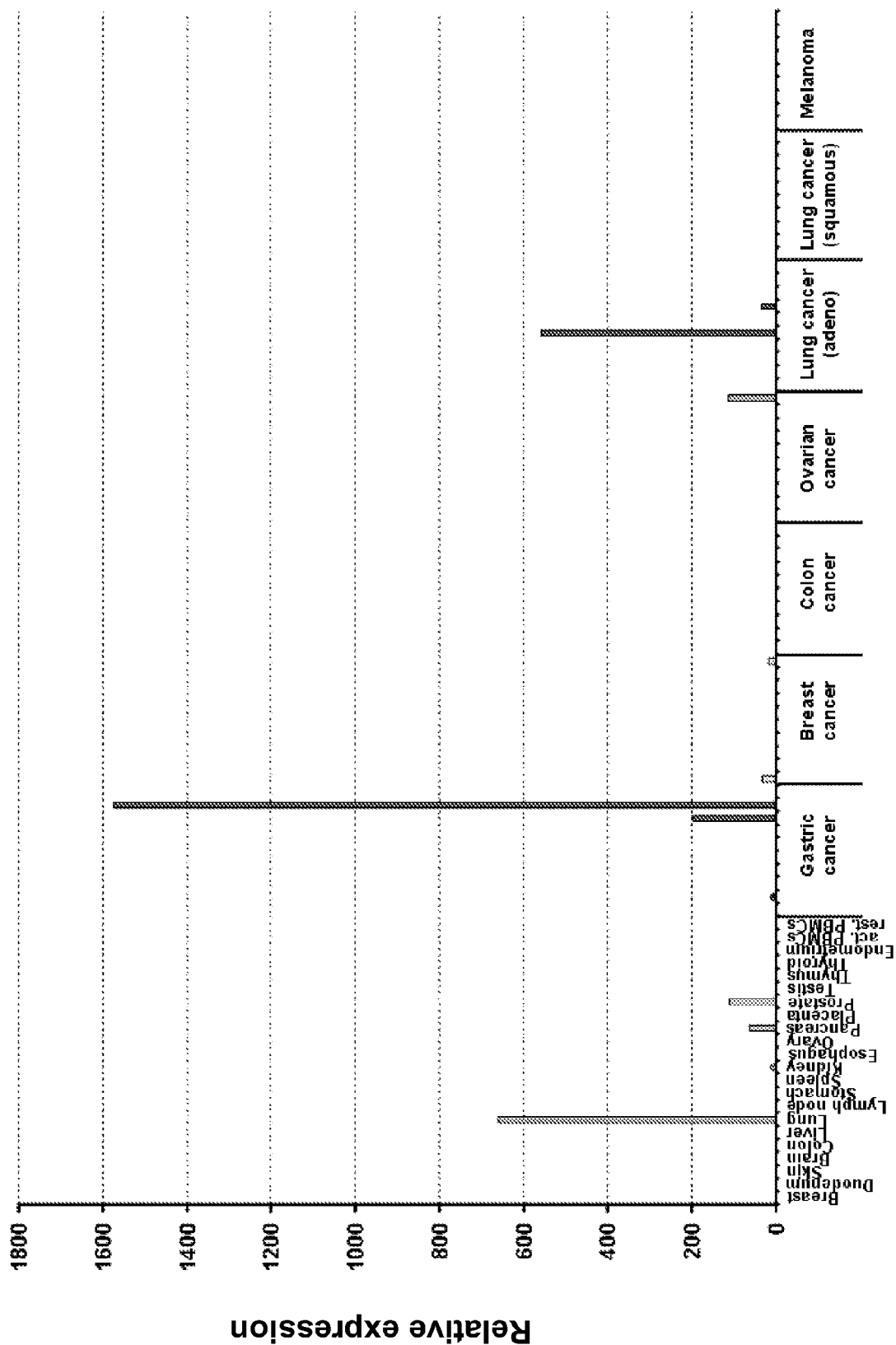
IDENTIFICATION OF TUMOR-ASSOCIATED MARKERS FOR DIAGNOSING OR MONITORING OVARIAN CANCER

RELATED APPLICATIONS

The present application is a continuation of International Patent Application No. PCT/EP08/08924, which was filed Oct. 22, 2008, claiming the benefit of priority to European Patent Application No. 07020730.3, which was filed on Oct. 23, 2007. The entire text of the aforementioned applications is incorporated herein by reference in its entirety.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[Not Applicable]

BACKGROUND OF THE INVENTION

The present technology relates to nucleic acids and encoded polypeptides which are expressed in cancers. The present technology also relates to agents which bind the polypeptides. The nucleic acids, polypeptides coded for by such nucleic acids and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, inter alia, in diagnostic and therapeutic contexts.

Despite interdisciplinary approaches and exhaustive use of classical therapeutic procedures, cancers are still among the leading causes of death.

More recent therapeutic concepts in cancer therapy aim at incorporating the patient's immune system into the overall therapeutic concept by using recombinant tumor vaccines and other specific measures such as antibody therapy. A prerequisite for the success of such a strategy is the recognition of tumor-specific or tumor-associated antigens or epitopes by the patient's immune system whose effector functions are to be interventionally enhanced.

Tumor cells biologically differ substantially from their nonmalignant cells of origin. These differences are due to genetic alterations acquired during tumor development and result, inter alia, also in the formation of qualitatively or quantitatively altered molecular structures in the cancer cells. Tumor-associated structures of this kind which are recognized by the specific immune system of the tumor-harboring host are referred to as tumor-associated antigens.

The specific recognition of tumor-associated antigens involves cellular and humoral mechanisms which are two functionally interconnected units: CD4$^+$ and CD8$^+$ T lymphocytes recognize the processed antigens presented on the molecules of the MHC (major histocompatibility complex) classes II and I, respectively, while B lymphocytes produce circulating antibody molecules which bind directly to unprocessed antigens. The potential clinical-therapeutical importance of tumor-associated antigens results from the fact that the recognition of antigens on neoplastic cells by the immune system leads to the initiation of cytotoxic effector mechanisms and, in the presence of T helper cells, can cause elimination of the cancer cells (Pardoll, *Nat. Med.* 4:525-31, 1998).

Antibody based cancer therapies have been successfully introduced into the clinic and have emerged as the most promising therapeutics in oncology over the last decade. Eight antibodies have been approved for treatment of neoplastic diseases, most of them, however in lymphoma and leukemia (Adams G P, Weiner L M, Nat Biotechnol 23:1147-57, 2005).

One of the challenges to be mastered for the advent of the next generation of upgraded antibody-based cancer therapeutics is the selection of appropriate target molecules, which is the key for a favorable toxicity/efficacy profile.

The search for genes tightly silenced in the vast majority of healthy tissues moves into the focus of attention the intriguing observation that genes of the gametogenic and/or trophoblastic lineage are frequently ectopically activated and robustly expressed in human cancer. Based on phenotypical similarities between germ cells, pregnancy trophoblast and cancer cells, John Beard proposed as much as 100 years ago a "trophoblastic theory of cancer" (Beard J, Lancet 1:1758-63, 1902; Gurchot C, Oncology 31:310-3, 1975). The discovery of the sporadic production of chorionic gonadotropin, alpha-fetoprotein, CEA and other trophoblastic hormones by cancer cells provided the first molecules shared between neoplastic and trophoblastic cells (Acevedo H F et al., Cancer 76:1467-75, 1995; Dirnhofer S 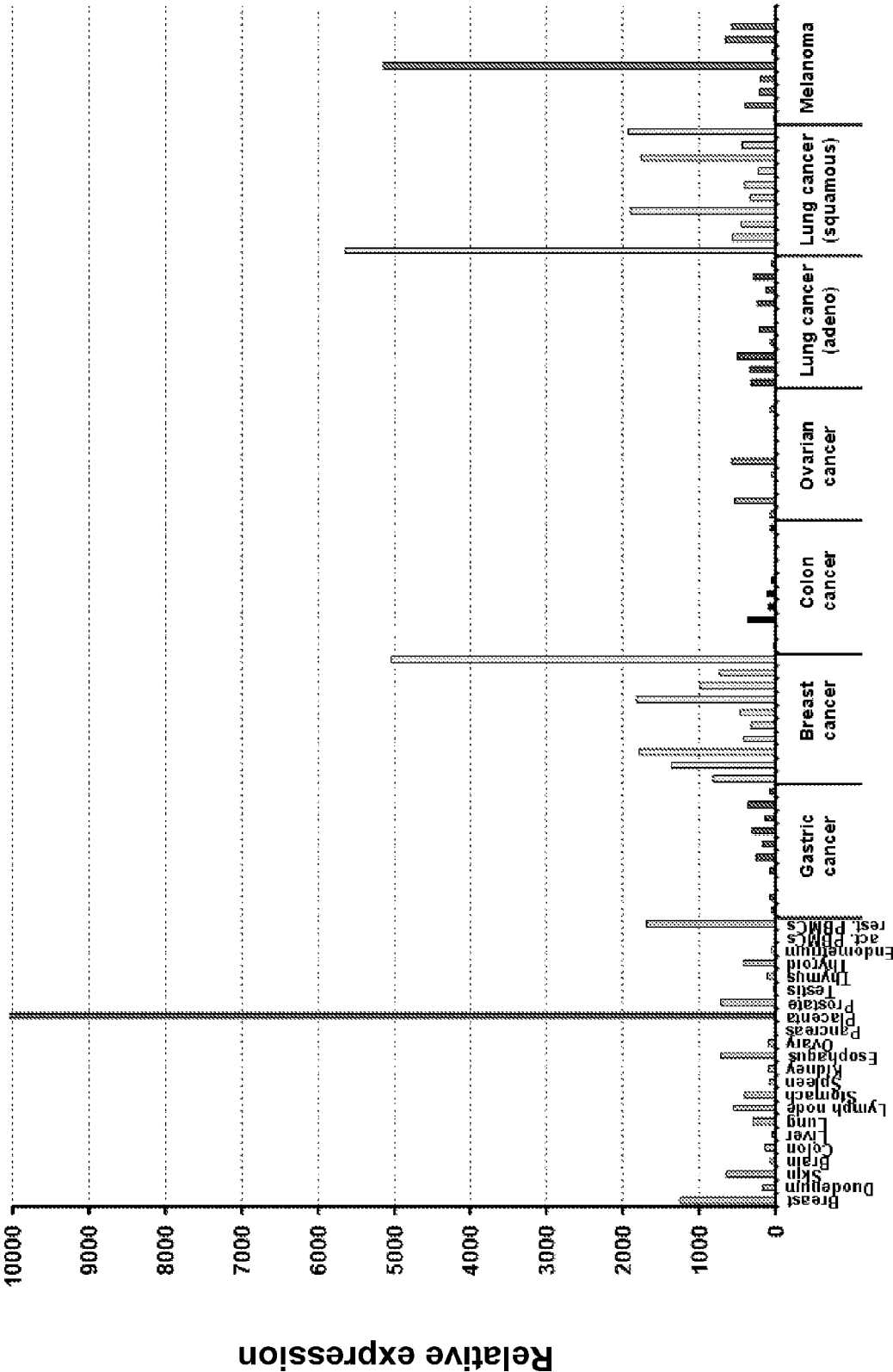et al., Hum Pathol 29:377-82, 1998; Gurchot C, Oncology 31:310-3, 1975; Iles R K, Chard T, J Urol 145:453-8, 1991; Laurence D J, Neville A M, Br J Cancer 26:335-55, 1972). The concept was reignited by the inauguration of the steadily growing so-called cancer/germline (CG) class of genes, which represents more than 100 members, each expressed in a variety of tumor types. The observation that entire trophoblastic and gametogenic programs escape transcriptional silencing and are ectopically activated in cancer cells (Koslowski M et al., Cancer Res 64:5988-93, 2004; Simpson A J et al., Nat Rev Cancer 5:615-25, 2005) indicates that within this class of genes with exquisitely selective tissue distribution, appropriate targets for mAB therapy may be found.

It was the object of the present technology to provide target structures for a diagnosis and therapy of cancers. This object is achieved by the subject matter of the claims.

BRIEF SUMMARY OF THE INVENTION

According to the present technology, placenta-specific genes are identified which are selectively or aberrantly expressed in tumor cells and thus, provide target structures for therapeutic and diagnostic approaches.

The nucleic acids identified according to the present technology to be selectively or aberrantly expressed in tumor cells are selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624 of the sequence listing, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). These nucleic acids are also termed "tumor-associated nucleic acids" herein.

In another aspect, the present technology relates to antigens encoded by the tumor-associated nucleic acids identified according to the present technology. Accordingly, the tumor-associated antigens identified according to the present technology have an amino acid sequence encoded by a nucleic acid which is selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624 of the sequence listing, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a)

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under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). In a preferred embodiment, the tumor-associated antigens identified according to the present technology comprise an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625 of the sequence listing, a part or derivative thereof.

If, according to the present technology, reference is made to nucleic acids comprising certain nucleic acid sequences or tumor-associated antigens comprising certain amino acid sequences this also includes embodiments wherein the nucleic acids or tumor-associated antigens consist of these certain nucleic acid sequences or amino acid sequences, respectively.

The present technology generally relates to the use of tumor-associated nucleic acids and tumor-associated antigens identified according to the present technology or of parts or derivatives thereof, of nucleic acids directed against said tumor-associated nucleic acids, of antibodies or T cells directed against the tumor-associated antigens identified according to the present technology or parts or derivatives thereof and/or of host cells expressing the tumor-associated antigens identified according to the present technology or parts or derivatives thereof for therapy, prophylaxis, diagnosis and/or monitoring of neoplastic diseases.

This may also involve the use of a combination of two or more of these nucleic acids, antigens, antibodies, T cells and/or host cells.

In those embodiments of the present technology relating to the use of antibodies directed against the tumor-associated antigens identified according to the present technology or parts or derivatives thereof also T cell receptors directed against the tumor-associated antigens identified according to the present technology or parts or derivatives thereof, optionally in a complex with MHC molecules, may be used.

Especially suitable for therapy, prophylaxis, diagnosis and/or monitoring is a part of the tumor-associated antigens identified according to the present technology which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof. Therefore, according to the present technology, a part of the tumor-associated antigens identified according to the present technology which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof, or a corresponding part of the nucleic acids coding for the tumor-associated antigens identified according to the present technology is preferred for therapy, prophylaxis, diagnosis and/or monitoring. Similarly the use of antibodies is preferred which are directed against a part of the tumor-associated antigens identified according to the present technology which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof.

Preferred diseases for a therapy, prophylaxis, diagnosis and/or monitoring are those in which one or more of the tumor-associated nucleic acids identified according to the present technology are selectively expressed or abnormally expressed. Particularly preferred diseases for a therapy, prophylaxis, diagnosis and/or monitoring are those in which one or more of the tumor-associated nucleic acids identified according to the present technology and/or one or more of the tumor-associated antigens encoded thereby are selectively expressed or abnormally expressed.

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In one aspect, the present technology relates to a pharmaceutical composition comprising an agent which recognizes a tumor-associated antigen identified according to the present technology or a nucleic acid coding for the tumor-associated antigen and which is preferably selective for cells which have expression or abnormal expression of a tumor-associated antigen identified according to the present technology.

In a further aspect, the present technology relates to a pharmaceutical composition comprising an agent which (I) inhibits expression or activity of a tumor-associated antigen identified according to the present technology, and/or (II) has tumor-inhibiting or tumor-destroying activity and is selective for cells expressing or abnormally expressing a tumor-associated antigen identified according to the present technology, and/or (III) when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen identified according to the present technology or a part thereof, such as a peptide epitope. In particular embodiments, said agent may cause induction of cell death, reduction in cell growth, damage to the cell membrane or secretion of cytokines and preferably have a tumor-inhibiting activity.

In one embodiment, the agent is an antisense nucleic acid which hybridizes selectively with the nucleic acid coding for the tumor-associated antigen. In a further embodiment, the agent is a siRNA preferably comprising a sense RNA strand and an antisense RNA strand, wherein the sense and antisense RNA strands form an RNA duplex, and wherein the sense RNA strand comprises a nucleotide sequence substantially identical to a target sequence of about 19 to about 25 contiguous nucleotides in a nucleic acid coding for the tumor-associated antigen, preferably mRNA coding for the tumor-associated antigen. In a further embodiment, the agent is an antibody which binds selectively to the tumor-associated antigen, in particular a complement-activated or toxin conjugated antibody which binds selectively to the tumor-associated antigen. In a preferred embodiment, the antibody which binds selectively to the tumor-associated antigen is coupled to a therapeutically useful substance and/or recruits natural or artificial effector mechanisms to said cell expressing or abnormally expressing said tumor-associated antigen. In a further embodiment, the agent is a cytotoxic T lymphocyte which recognizes the tumor-associated antigen or a part thereof bound by an MHC molecule on a cell and lyses the cells labeled in this way. In a further embodiment, the agent is a T helper lymphocyte which recognizes the tumor-associated antigen or a part thereof bound by an MHC molecule on a cell and enhances effector functions of other cells specifically recognizing said tumor-associated antigen or a part thereof.

In a further embodiment, the agent comprises two or more agents which each recognize different tumor-associated antigens or different nucleic acids coding for tumor-associated antigens and/or inhibit expression or activity of different tumor-associated antigens, and/or have tumor-inhibiting or tumor-destroying activity and are selective for cells expressing or abnormally expressing different tumor-associated antigens, and/or when administered, selectively increase the amount of complexes between MHC molecules and different tumor-associated antigens or parts thereof, wherein at least one of said different tumor-associated antigens is a tumor-associated antigen identified according to the present technology.

Preferably, a tumor-associated antigen selectively limited to tumors serves as a label for recruiting effector mechanisms to this specific location. In this aspect, the present technology includes embodiments wherein the agent itself does not have

an ability to inhibit activity of a tumor-associated antigen or a tumor-inhibiting or tumor-destroying activity but mediates such effect, in particular by recruiting effector mechanisms, in particular those having cell damaging potential, to a specific location, in particular a tumor or tumor cells.

Preferably, said cells expressing or abnormally expressing a tumor-associated antigen identified according to the present technology are non-placenta cells.

The activity of a tumor-associated antigen identified according to the present technology can be any activity of a protein or a peptide. In one embodiment this activity is an enzymatic activity.

According to the present technology the phrase "inhibit expression or activity" includes a complete or essentially complete inhibition of expression or activity and a reduction in expression or activity.

The agent which, when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen identified according to the present technology or a part thereof comprises one or more components selected from the group consisting of (i) the tumor-associated antigen or a part thereof, (ii) a nucleic acid which codes for said tumor-associated antigen or a part thereof, (iii) a host cell which expresses said tumor-associated antigen or a part thereof, and (iv) isolated complexes between peptide epitopes from said tumor-associated antigen and an MHC molecule.

The present technology furthermore relates to a pharmaceutical composition which comprises one or more components selected from the group consisting of (i) a tumor-associated antigen identified according to the present technology or a part thereof, (ii) a nucleic acid which codes for a tumor-associated antigen identified according to the present technology or a part thereof, (iii) an antibody which binds to a tumor-associated antigen identified according to the present technology or to a part thereof, (iv) an antisense nucleic acid which hybridizes specifically with a tumor-associated nucleic acid identified according to the present technology/a nucleic acid coding for a tumor-associated antigen identified according to the present technology, (v) an siRNA directed against a tumor-associated nucleic acid identified according to the present technology/a nucleic acid coding for a tumor-associated antigen identified according to the present technology, (vi) a host cell which expresses a tumor-associated antigen identified according to the present technology or a part thereof, and (vii) isolated complexes between a tumor-associated antigen identified according to the present technology or a part thereof and an MHC molecule.

In one embodiment, a nucleic acid coding for a tumor-associated antigen identified according to the present technology or a part thereof is present in the pharmaceutical composition in an expression vector and functionally linked to a promoter. In a further embodiment, a nucleic acid coding for a tumor-associated antigen identified according to the present technology or a part thereof is present in the pharmaceutical composition in a virus as further described below.

A host cell present in a pharmaceutical composition of the present technology may secrete the tumor-associated antigen or the part thereof, may express it on the surface and preferably may additionally express an MHC molecule which binds to said tumor-associated antigen or said part thereof. In one embodiment, the host cell expresses the MHC molecule endogenously. In a further embodiment, the host cell expresses the MHC molecule and/or the tumor-associated antigen or the part thereof in a recombinant manner. The host cell is preferably nonproliferative. In a preferred embodi-

ment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

In a further embodiment, an antibody present in a pharmaceutical composition of the present technology is a monoclonal antibody. In further embodiments, the antibody is a chimeric or humanized antibody, a fragment of an antibody or a synthetic antibody. The antibody may be coupled to a therapeutically or diagnostically useful agent also termed therapeutic or diagnostic agent herein.

An antisense nucleic acid present in a pharmaceutical composition of the present technology may comprise a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of the nucleic acid coding for the tumor-associated antigen identified according to the present technology.

In further embodiments, a tumor-associated antigen or a part thereof, provided by a pharmaceutical composition of the present technology either directly or via expression of a nucleic acid, binds to MHC molecules on the surface of cells, said binding preferably causing a cytolytic response and/or inducing cytokine release.

A pharmaceutical composition of the present technology may comprise a pharmaceutically compatible carrier and/or an adjuvant.

A pharmaceutical composition of the present technology is preferably used for the treatment or prevention of a disease characterized by selective expression or abnormal expression of a tumor-associated nucleic acid and/or tumor-associated antigen. In a preferred embodiment, the disease is a neoplastic disease, preferably cancer.

In a preferred embodiment, the pharmaceutical composition of the present technology is in the form of a vaccine which may be used therapeutically or prophylactically. Such vaccine preferably comprises a tumor-associated antigen identified according to the present technology or a part thereof, and/or a nucleic acid which codes for a tumor-associated antigen identified according to the present technology or a part thereof. In particular embodiments, the nucleic acid is present in a virus or host cell.

The present technology furthermore relates to methods of treating, preventing, diagnosing or monitoring, i.e. determining the regression, progression, course and/or onset of, a disease characterized by expression or abnormal expression of one of more tumor-associated nucleic acids identified according to the present technology, preferably also resulting in expression or abnormal expression of one of more tumor-associated antigens identified according to the present technology, preferably a neoplastic disease, in particular cancer. In one embodiment, the treatment or prevention comprises administering a pharmaceutical composition of the present technology.

The methods of diagnosing and/or methods of monitoring according to the present technology generally concern the detection of and/or determination of the quantity of one or more parameters selected from the group consisting of (i) a tumor-associated nucleic acid identified according to the present technology, or a part thereof, (ii) a tumor-associated antigen identified according to the present technology, or a part thereof, (iii) an antibody against a tumor-associated antigen identified according to the present technology or a part thereof, and (iv) T lymphocytes, preferably cytotoxic or T helper lymphocytes, which are specific for a tumor-associated antigen identified according to the present technology or a part thereof and/or a complex between the tumor-associated antigen or a part thereof and an MHC molecule, in a biological sample isolated from a patient, preferably from a patient having said disease, being suspected of having or falling ill with said disease or having a potential for said disease. Means

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for accomplishing said detection and/or determination of the quantity are described herein and will be apparent to the skilled person.

Preferably, the presence of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes and/or a quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased compared to a patient without said disease is indicative for the presence of said disease or a potential for a development of said disease.

The methods of diagnosing and/or monitoring of the present technology also include embodiments wherein by detection or determination of the quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes it is possible to assess and/or prognose the metastatic behavior of said disease, wherein, preferably, the presence of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes and/or a quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased compared to a patient without said disease or without a metastasis of said disease is indicative for a metastatic behavior of said disease or a potential for a metastatic behavior of said disease.

In particular embodiments, said detection or determination of the quantity comprises (i) contacting a biological sample with an agent which binds specifically to said tumor-associated nucleic acid or said part thereof, to said tumor-associated antigen or said part thereof, to said antibody or to said T lymphocytes, and (ii) detecting the formation of or determining the amount of a complex between the agent and the nucleic acid or the part thereof, the tumor-associated antigen or the part thereof, the antibody, or the T lymphocytes.

In one embodiment, the disease is characterized by expression or abnormal expression of two or more different tumor-associated nucleic acids preferably also resulting in expression or abnormal expression of two or more different tumor-associated antigens and a detection or determination of the quantity comprises a detection or determination of the quantity of two or more different tumor-associated nucleic acids or of parts thereof, of two or more different tumor-associated antigens or of parts thereof, of two or more antibodies binding to said two or more different tumor-associated antigens or to parts thereof and/or of two or more T lymphocytes specific for said two or more different tumor-associated antigens or parts thereof, or complexes thereof with MHC molecules. In a further embodiment, the biological sample isolated from the patient is compared to a comparable normal biological sample.

The methods of monitoring according to the present technology preferably comprise a detection of and/or determination of the quantity of one or more of the parameters mentioned above in a first sample at a first point in time and in a further sample at a second point in time, wherein the course of the disease is determined by comparing the two samples.

Preferably, a level of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased in a sample compared to a sample taken earlier from a patient indicates that the patient has developed or is about to develop cancer and/or a metastasis of cancer and/or a relapse of cancer. Preferably, a level of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is decreased in a sample compared to a sample taken earlier from a patient

indicates regression of cancer and/or a metastasis of cancer in said patient and thus, preferably indicates a successful cancer therapy.

According to the present technology, detection of a nucleic acid or of a part thereof or determining the quantity of a nucleic acid or of a part thereof may be carried out using a oligo- or polynucleotide probe which hybridizes specifically to said nucleic acid or said part thereof or may be carried out by selective amplification of said nucleic acid or said part thereof, e.g. by means of PCR amplification. In one embodiment, the oligo- or polynucleotide probe comprises a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of said nucleic acid.

In particular embodiments, the tumor-associated antigen or the part thereof which is to be detected or the quantity of which is to be determined in the methods of the present technology is present intracellularly, on the cell surface or in a complex with an MHC molecule.

According to the present technology, detection of a tumor-associated antigen or of a part thereof or determining the quantity of a tumor-associated antigen or of a part thereof may be carried out using an antibody binding specifically to said tumor-associated antigen or said part thereof.

According to the present technology, detection of an antibody or determining the quantity of an antibody may be carried out using a protein or peptide binding specifically to said antibody.

According to the present technology, detection of or determining the quantity of T lymphocytes which are specific for a tumor-associated antigen or a part thereof and/or a complex thereof with an MHC molecule may be carried out using a cell presenting the complex between said tumor-associated antigen or said part thereof and an MHC molecule. T lymphocytes may additionally be detected by detecting their proliferation, their cytokine production, and their cytotoxic activity triggered by specific stimulation with a complex of an MHC molecule and a tumor-associated antigen or a part thereof. T lymphocytes may also be detected with aid of a recombinant MHC molecule or a complex of two or more MHC molecules loaded with immunogenic fragments of one or more tumor-associated antigens.

An agent which is used for detection or determining the quantity in the methods of the present technology such as a oligo- or polynucleotide probe, an antibody, a protein or peptide or a cell is preferably labeled in a detectable manner, in particular by a detectable marker such as a radioactive marker or an enzymic marker.

In a particular aspect, the present technology relates to a method of treating, preventing, diagnosing or monitoring a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the present technology, which method comprises administering an antibody which binds to said tumor-associated antigen or to a part thereof and which is coupled to a therapeutic or diagnostic agent. The antibody may be a monoclonal antibody. In further embodiments, the antibody is a chimeric or humanized antibody or a fragment of an antibody.

In certain embodiments, the methods of the present technology of diagnosing or monitoring a disease are performed with a biological sample containing or suspected of containing disseminating tumor cells or metastatic tumor cells. Such biological samples include, for example, blood, serum, bone marrow, sputum, bronchial aspirate, and/or bronchial lavage. Preferably, the methods of the present technology of diagnosing or monitoring a disease are performed with a biological sample not containing placental cells and, in particular, being a non-placenta biological sample isolated from a subject.

In one particular aspect, the present technology relates to a method of treating a patient having a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the present technology, which method comprises (i) providing a sample containing immunoreactive cells, either obtained from said patient or from another individual of the same species, in particular a healthy individual, or an individual of a different species, (ii) contacting said sample with a host cell expressing said tumor-associated antigen or a part thereof, under conditions which favor production of cytolytic T cells against said tumor-associated antigen or a part thereof, and (iii) introducing the cytolytic T cells into the patient in an amount suitable for lysing cells expressing the tumor-associated antigen or a part thereof. In one embodiment, the method includes cloning of the T cell receptor of cytolytic T cells obtained and transferring the nucleic acid coding for the T cell receptor to T cells, either obtained from said patient or from another individual of the same species, in particular a healthy individual, or an individual of a different species, which T cells thus receive the desired specificity and, as under (iii), may be introduced into the patient.

In one embodiment, the host cell endogenously expresses an MHC molecule. In a further embodiment, the host cell recombinantly expresses an MHC molecule and/or the tumor-associated antigen or the part thereof. Preferably, the host cell presents the tumor-associated antigen or the part thereof by MHC molecules on its surface. The host cell is preferably nonproliferative. In a preferred embodiment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

The present technology also relates to a method of treating a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the present technology, which method comprises (i) identifying cells from the patient which express abnormal amounts of the tumor-associated antigen, (ii) isolating a sample of said cells, (iii) culturing said cells, and (iv) introducing said cells into the patient in an amount suitable for triggering an immune response to the cells.

The present technology furthermore relates to a nucleic acid selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In a further aspect, the present technology relates to a recombinant nucleic acid molecule, in particular DNA or RNA molecule, which comprises a nucleic acid of the present technology.

The present technology also relates to host cells which contain a nucleic acid or recombinant nucleic acid molecule of the present technology.

The host cell may also comprise a nucleic acid coding for a MHC molecule. In one embodiment, the host cell endogenously expresses the MHC molecule. In a further embodiment, the host cell recombinantly expresses the MHC molecule and/or the nucleic acid or recombinant nucleic acid molecule of the present technology or a part thereof. Preferably, the host cell is nonproliferative. In a preferred embodiment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

In a further embodiment, the present technology relates to oligonucleotides which hybridize with a nucleic acid identified according to the present technology and which may be used as genetic probes or as "antisense" molecules. Nucleic acid molecules in the form of oligonucleotide primers or competent probes, which hybridize with a nucleic acid identified according to the present technology or parts thereof, may be used for detecting said nucleic acid and/or finding nucleic acids which are homologous to said nucleic acid identified according to the present technology, e.g. by PCR amplification, Southern and Northern hybridization. Hybridization may be carried out under low stringency, more preferably under medium stringency and most preferably under high stringency conditions.

In a further aspect, the present technology relates to a protein or peptide which is encoded by a nucleic acid selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). In a preferred embodiment, the protein or peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625 of the sequence listing, a part or derivative thereof.

In a further aspect, the present technology relates to an immunogenic fragment of a tumor-associated antigen identified according to the present technology. Said fragment preferably binds to a MHC molecule or an antibody, preferably to a human HLA receptor or a human antibody. According to the present technology, a part or fragment preferably comprises a sequence of at least 5, at least 6, in particular at least 8, at least 10, at least 12, at least 15, at least 20, at least 30 or at least 50, amino acids.

In a further aspect, the present technology relates to an agent which binds to a tumor-associated antigen identified according to the present technology or to a part thereof. In a preferred embodiment, the agent is a protein or peptide, in particular an antibody, a T cell receptor or an MHC molecule. In further embodiments, the antibody is a monoclonal, chimeric, or humanized antibody, an antibody produced by combinatory techniques, or a fragment of an antibody. In one preferred embodiment, the present technology relates to an antibody which binds selectively to a complex of (i) a tumor-associated antigen identified according to the present technology or a part thereof and (ii) an MHC molecule to which said tumor-associated antigen identified according to the present technology or said part thereof binds, with said antibody not binding to (i) or (ii) alone.

According to the present technology, the term "binding" preferably relates to a specific binding. "Specific binding" means that an agent such as an antibody binds stronger to a target such as an epitope for which it is specific compared to the binding to another target. An agent binds stronger to a first target compared to a second target if it binds to the first target with a dissociation constant (K_D) which is lower than the dissociation constant for the second target. Preferably the dissociation constant (K_D) for the target to which the agent binds specifically is more than 10-fold, preferably more than 20-fold, more preferably more than 50-fold, even more preferably more than 100-fold, 200-fold, 500-fold or 1000-fold

lower than the dissociation constant (K_D) for the target to which the agent does not bind specifically.

Such specific antibodies may, for example, be obtained by immunization using the aforementioned peptides.

The present technology furthermore relates to a conjugate between an agent of the present technology which binds to a tumor-associated antigen identified according to the present technology or to a part thereof or an antibody of the present technology and a therapeutic or diagnostic agent. In one embodiment, the therapeutic or diagnostic agent is a toxin.

In a further aspect, the present technology relates to a kit for detecting a disease characterized by expression or abnormal expression of one of more tumor-associated nucleic acids identified according to the present technology, preferably also resulting in expression or abnormal expression of one of more tumor-associated antigens identified according to the present technology, preferably a neoplastic disease, in particular cancer, which kit comprises agents for detection or determining the quantity (i) of the tumor-associated nucleic acid or of a part thereof, (ii) of the tumor-associated antigen or of a part thereof, (iii) of antibodies which bind to the tumor-associated antigen or to a part thereof, and/or (iv) of T cells which are specific for the tumor-associated antigen or a part thereof or a complex thereof with an MHC molecule. Such agents are described herein above.

In one embodiment, the present technology relates to a pharmaceutical composition which comprises an agent that (I) inhibits expression or activity of a tumor-associated antigen and/or (II) has tumor-inhibiting activity, and is selective for cells expressing or abnormally expressing a tumor-associated antigen and/or (III) when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen or a part thereof, the tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In another embodiment, the present technology relates to a pharmaceutical composition which comprises one or more components selected from the group consisting of: (i) a tumor-associated antigen or a part thereof, (ii) a nucleic acid which codes for a tumor-associated antigen or a part thereof, (iii) an antibody which binds to a tumor-associated antigen or a part thereof, (iv) an antisense nucleic acid which hybridizes specifically with a nucleic acid coding for a tumor-associated antigen, (v) an siRNA directed against a nucleic acid coding for a tumor-associated antigen, (vi) a host cell which expresses a tumor-associated antigen or a part thereof, and (vii) isolated complexes between a tumor-associated antigen or a part thereof and an MHC molecule, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic

acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In yet another embodiment, the present technology relates to a method of diagnosing or monitoring a cancer disease which comprises detecting or determining the quantity (i) of a tumor-associated nucleic acid or of a part thereof, and/or (ii) of a tumor-associated antigen or of a part thereof, and/or (iii) of an antibody to the tumor-associated antigen or a part thereof and/or (iv) of T lymphocytes which are specific to the tumor-associated antigen or to a part thereof in a biological sample isolated from a patient, said tumor-associated nucleic acid being selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

In a further embodiment, the present technology relates to a method of treating or preventing a disease characterized by expression or abnormal expression of a tumor-associated antigen which comprises administration of a pharmaceutical composition of the present technology, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In yet another embodiment, the present technology relates to a method of treating, preventing, diagnosing or monitoring a disease characterized by expression or abnormal expression of a tumor-associated antigen which comprises administering an antibody that binds to said tumor-associated antigen or to a part thereof and is coupled to a therapeutic or diagnostic agent, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

Another embodiment of the present technology relates to a method of treating a patient having a disease characterized by expression or abnormal expression of a tumor-associated antigen which comprises: (i) providing a sample containing immunoreactive cells, (ii) contacting said sample with a host cell expressing said tumor-associated antigen or a part thereof, under conditions which favor production of cytolytic or cytokine-releasing T cells against said tumor-associated antigen or said part thereof, and (iii) introducing the cytolytic or cytokine-releasing T cells into the patient in an amount

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suitable for lysing cells expressing the tumor-associated antigen or a part thereof, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

An additional embodiment of the present technology relates to a method of inhibiting the development of cancer in a patient which comprises administering an effective amount of a pharmaceutical composition of the present technology.

In yet another embodiment, the present technology relates to an agent, which binds specifically to a protein or polypeptide or to a part thereof, said protein or polypeptide being encoded by a nucleic acid selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In an additional embodiment, the present technology relates to an antibody, which binds selectively to a complex of: (i) a protein or polypeptide or a part thereof and (ii) an MHC molecule to which said protein or polypeptide or said part thereof binds, with said antibody not binding to (i) or (ii) alone and said protein or polypeptide being encoded by a nucleic acid selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

In yet another embodiment, the present technology relates to a kit for detecting cancer, which comprises agents for detecting or determining the quantity of (i) of a tumor-associated nucleic acid or of a part thereof, and/or (ii) of a tumor-associated antigen or of a part thereof, and/or (iii) of antibodies which bind to the tumor-associated antigen or to a part thereof, and/or (iv) of T cells which are specific for a complex between the tumor-associated antigen or a part thereof and an MHC molecule, said tumor-associated nucleic acid being selected from the group consisting of: (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

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BRIEF DESCRIPTION OF SEVERAL VIEWS OF THE DRAWINGS

FIG. 1. Expression of a tumor-associated nucleic acid identified according to the present technology in normal tissues and cancer tissue. Significant expression of the nucleic acid sequence according to SEQ ID NO:540 was found only in placenta tissue and mamma carcinomas.

FIG. 2. Quantitative expression of a tumor-associated nucleic acid identified according to the present technology in normal tissues and cancer tissue. Quantitative RT-PCR showed selective expression of the nucleic acid sequence according to SEQ ID NO:540 in placenta tissue and mamma carcinomas.

FIG. 3. Quantitative expression of SEQ ID NO:540 mRNA in MCF-7 breast cancer cells. Real-time RT-PCR 24 h after transfection with siRNA oligos showed that both SEQ ID NO:540-specific siRNAs (siRNA#1 (SEQ ID NO:630, 631), siRNA#2 (SEQ ID NO:632, 633)) induce robust silencing of SEQ ID NO:540 expression.

FIG. 4. Silencing of SEQ ID NO:540 expression by transfection with siRNA oligos results in impaired proliferation of MCF-7 breast cancer cells. Proliferation was quantified 96 h after transfection with siRNAs by measuring incorporation of BrdU in newly synthesized DNA strands. These results show that SEQ ID NO:540 is a positive factor for the proliferation of breast cancer cells.

FIG. 5. Quantitative expression of SEQ ID NO:541 in normal tissues and cancer tissue. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:541 in lung cancer.

FIG. 6. Quantitative expression of SEQ ID NO:545 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:545 in malignant melanomas.

FIG. 7. Quantitative expression of SEQ ID NO:549 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:549 in ovarian cancer.

FIG. 8. Quantitative expression of SEQ ID NO:553 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:553 in colon cancer and ovarian cancer.

FIG. 9. Quantitative expression of SEQ ID NO:557 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:557 in breast cancer.

FIG. 10. Quantitative expression of SEQ ID NO:560 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:560 in colon cancer and ovarian cancer.

FIG. 11. Quantitative expression of SEQ ID NO:563 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:563 in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

FIG. 12. Quantitative expression of SEQ ID NO:566 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:566 in gastric cancer, breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

FIG. 13. Quantitative expression of SEQ ID NO:570 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:570 in ovarian cancer, lung cancer and melanoma.

FIG. **14**. Quantitative expression of SEQ ID NO:574 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:574 in lung cancer and melanoma.

FIG. **15**. Quantitative expression of SEQ ID NO:577 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:577 in gastric cancer, breast cancer and lung cancer.

FIG. **16**. Quantitative expression of SEQ ID NO:580 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:580 in ovarian cancer and lung cancer.

FIG. **17**. Quantitative expression of SEQ ID NO:583 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:583 in colon cancer, ovarian cancer and lung cancer.

FIG. **18**. Quantitative expression of SEQ ID NO:587 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:587 in lung cancer.

FIG. **19**. Quantitative expression of SEQ ID NO:591 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:591 in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

FIG. **20**. Quantitative expression of SEQ ID NO:595 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:595 in gastric cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

FIG. **21**. Quantitative expression of SEQ ID NO:599 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:599 in gastric cancer, breast cancer, lung cancer and melanoma.

FIG. **22**. Quantitative expression of SEQ ID NO:602 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:602 in ovarian cancer and lung cancer.

FIG. **23**. Quantitative expression of SEQ ID NO:606 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:606 in gastric cancer, colon cancer and lung cancer.

FIG. **24**. Quantitative expression of SEQ ID NO:610 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:610 in gastric cancer, breast cancer and lung cancer.

FIG. **25**. Quantitative expression of SEQ ID NO:613 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:613 in breast cancer, lung cancer and melanoma.

FIG. **26**. Quantitative expression of SEQ ID NO:617 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:617 in lung cancer and melanoma.

FIG. **27**. Quantitative expression of SEQ ID NO:620 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:620 in ovarian cancer and melanoma.

FIG. **28**. Quantitative expression of SEQ ID NO:624 in normal tissues and cancer tissues. Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:624 in gastric cancer and lung cancer.

DETAILED DESCRIPTION OF THE INVENTION

A reference herein to a range of numerical values is to be understood so as to specify and mention each of the individual numerical values comprised by said range. For example, a reference to SEQ ID NOs: 1-540 is to be understood so as to refer to each and every of the following individual SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, and 540.

According to the present technology, a "reference" such as a reference sample or reference organism may be used to correlate and compare the results obtained in the methods of the present technology from a test sample or test organism, i.e. a patient. Typically the reference organism is a healthy organism, in particular an organism which does not suffer from cancer.

A "reference value" can be determined from a reference empirically by measuring a sufficiently large number of references. Preferably the reference value is determined by measuring at least 2, preferably at least 3, preferably at least 5, preferably at least 8, preferably at least 12, preferably at least 20, preferably at least 30, preferably at least 50, or preferably at least 100 references.

According to the present technology, a nucleic acid is preferably deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). Nucleic acids comprise according to the present tech-

nology genomic DNA, cDNA, mRNA, recombinantly produced and chemically synthesized molecules. According to the present technology, a nucleic acid may be present as a single-stranded or double-stranded and linear or covalently circularly closed molecule.

The terms "tumor-associated nucleic acid identified according to the present technology" and "nucleic acid encoding a tumor-associated antigen identified according to the present technology" have similar meanings. However, the different terms are used herein to account for the fact that in some embodiments only the expression of nucleic acid, in particular mRNA, is of relevance while the expression of protein is not a critical factor.

As used herein, the term "RNA" means a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2'-position of a beta-D-ribo-furanose moiety. The term includes double stranded RNA, single stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of a RNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in RNA molecules can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

If reference is made herein to the detection of or the determination of the quantity of a nucleic acid, the nucleic acid which is actually to be detected or the quantity of which is actually to be determined is preferably mRNA. However, it should be understood that this may also include embodiments wherein mRNA is detected or the quantity of mRNA is determined indirectly. For example, mRNA may be transformed into cDNA and the cDNA detected or its quantity determined. mRNA is given herein as the cDNA equivalent. One skilled in the art would understand that the cDNA sequence is equivalent to the mRNA sequence, and can be used for the same purpose herein, e.g., the generation of probes hybridizing to the nucleic acid to be detected. Thus, if reference is made herein to the sequences shown in the sequence listing this is also to include the RNA equivalents of said sequences.

The nucleic acids described according to the present technology have preferably been isolated. The term "isolated nucleic acid" means according to the present technology that the nucleic acid was (i) amplified in vitro, for example by polymerase chain reaction (PCR), (ii) recombinantly produced by cloning, (iii) purified, for example by cleavage and gel-electrophoretic fractionation, or (iv) synthesized, for example by chemical synthesis. An isolated nucleic acid is a nucleic acid which is available for manipulation by recombinant DNA techniques.

A degenerate nucleic acid according to the present technology is a nucleic acid that differs from a reference nucleic acid in codon sequence due to the degeneracy of the genetic code.

"Derivative" of a nucleic acid means according to the present technology that single or multiple such as at least 2, at least 4, or at least 6 and preferably up to 3, up to 4, up to 5, up to 6, up to 10, up to 15, or up to 20 nucleotide substitutions, deletions and/or additions are present in said nucleic acid. Furthermore, the term "derivative" also comprises chemical derivatization of a nucleic acid on a nucleotide base, on the sugar or on the phosphate. The term "derivative" also com-

prises nucleic acids which contain nucleotides and nucleotide analogs not occurring naturally.

Preferably the degree of identity between a specific nucleic acid sequence described herein and a nucleic acid sequence which is a derivative of said specific nucleic acid sequence, which hybridizes with said specific nucleic acid sequence and/or which is degenerate with respect to said specific nucleic acid sequence will be at least 70%, preferably at least 75%, preferably at least 80%, more preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%. The degree of identity is preferably given for a region of at least about 30, at least about 50, at least about 70, at least about 90, at least about 100, at least about 150, at least about 200, at least about 250, at least about 300, or at least about 400 nucleotides. In preferred embodiments, the degree of identity is given for the entire length of the reference nucleic acid sequence, such as the nucleic acid sequences given in the sequence listing.

A nucleic acid is "complementary" to another nucleic acid if the two sequences are capable of hybridizing and forming a stable duplex with one another, with hybridization preferably being carried out under conditions which allow specific hybridization between polynucleotides (stringent conditions). Stringent conditions are described, for example, in Molecular Cloning: A Laboratory Manual, J. Sambrook et al., Editors, 2nd Edition, Cold Spring Harbor Laboratory press, Cold Spring Harbor, N.Y., 1989 or Current Protocols in Molecular Biology, F. M. Ausubel et al., Editors, John Wiley & Sons, Inc., New York and refer, for example, to hybridization at 65° C. in hybridization buffer (3.5×SSC, 0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% bovine serum albumin, 2.5 mM NaH_2PO_4 (pH 7), 0.5% SDS, 2 mM EDTA). SSC is 0.15 M sodium chloride/0.15 M sodium citrate, pH 7. After hybridization, the membrane to which the DNA has been transferred is washed, for example, in 2×SSC at room temperature and then in 0.1-0.5×SSC/0.1×SDS at temperatures of up to 68° C.

A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" or "fully complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. Preferably, the degree of complementarity according to the present technology is at least 70%, preferably at least 75%, preferably at least 80%, more preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%.

"Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions. "Sequence identity" between two polypeptide or nucleic acid sequences indicates the percentage of amino acids or nucleotides that are identical between the sequences.

The term "percentage identity" is intended to denote a percentage of nucleotides or of amino acid residues which are identical between the two sequences to be compared, obtained after the best alignment, this percentage being purely statistical and the differences between the two sequences being distributed randomly and over their entire length. Sequence comparisons between two nucleotide or amino acid sequences are conventionally carried out by comparing these sequences after having aligned them optimally, said comparison being carried out by segment or by "window of comparison" in order to identify and compare local regions

of sequence similarity. The optimal alignment of the sequences for comparison may be produced, besides manually, by means of the local homology algorithm of Smith and Waterman, 1981, Ads App. Math. 2, 482, by means of the local homology algorithm of Neddleman and Wunsch, 1970, J. Mol. Biol. 48, 443, by means of the similarity search method of Pearson and Lipman, 1988, Proc. Natl Acad. Sci. USA 85, 2444, or by means of computer programs which use these algorithms (GAP, BESTFIT, FASTA, BLAST P, BLAST N and TFASTA in Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.).

The percentage identity is calculated by determining the number of identical positions between the two sequences being compared, dividing this number by the number of positions compared and multiplying the result obtained by 100 so as to obtain the percentage identity between these two sequences.

In one embodiment, a nucleic acid sequence which is a derivative of a specific nucleic acid sequence, which is degenerate with respect to a specific nucleic acid sequence or which is a part of a specific nucleic acid sequence has a relevant function and/or activity of the specific nucleic acid sequence, i.e. it may encode a protein or peptide having the same activity or immunological properties as the protein or peptide encoded by the specific nucleic acid sequence and, in one embodiment, encodes the same protein or peptide.

Nucleic acids coding for tumor-associated antigens may, according to the present technology, be present alone or in combination with other nucleic acids, in particular heterologous nucleic acids. In preferred embodiments, a nucleic acid is functionally linked to expression control sequences or regulatory sequences which may be homologous or heterologous with respect to said nucleic acid. A coding sequence and a regulatory sequence are "functionally" linked to one another, if they are covalently linked to one another in such a way that expression or transcription of said coding sequence is under the control or under the influence of said regulatory sequence. If the coding sequence is to be translated into a functional protein, then, with a regulatory sequence functionally linked to said coding sequence, induction of said regulatory sequence results in transcription of said coding sequence, without causing a frame shift in the coding sequence or said coding sequence not being capable of being translated into the desired protein or peptide.

The term "expression control sequence" or "regulatory sequence" comprises according to the present technology promoters, enhancers and other control elements which regulate expression of a gene. In particular embodiments of the present technology, the expression control sequences can be regulated. The exact structure of regulatory sequences may vary as a function of the species or cell type, but generally comprises 5'untranscribed and 5'untranslated sequences which are involved in initiation of transcription and translation, respectively, such as TATA box, capping sequence, CAAT sequence, and the like. More specifically, 5'untranscribed regulatory sequences comprise a promoter region which includes a promoter sequence for transcriptional control of the functionally linked gene. Regulatory sequences may also comprise enhancer sequences or upstream activator sequences.

According to the present technology, a nucleic acid may furthermore be present in combination with another nucleic acid which codes for a peptide controlling secretion of the protein or peptide encoded by said nucleic acid from a host cell. According to the present technology, a nucleic acid may also be present in combination with another nucleic acid which codes for a peptide causing the encoded protein or peptide to be anchored on the cell membrane of the host cell or compartmentalized into particular organelles of said cell. Similarly, a combination with a nucleic acid is possible which represents a reporter gene or any "tag".

In a preferred embodiment, a recombinant nucleic acid molecule is according to the present technology a vector, where appropriate with a promoter, which controls expression of a nucleic acid, for example a nucleic acid coding for a tumor-associated antigen identified according to the present technology. The term "vector" is used here in its most general meaning and comprises any intermediary vehicle for a nucleic acid which enables said nucleic acid, for example, to be introduced into prokaryotic and/or eukaryotic cells and, where appropriate, to be integrated into a genome. Vectors of this kind are preferably replicated and/or expressed in the cells. An intermediary vehicle may be adapted, for example, to the use in electroporation, in bombardment with microprojectiles, in liposomal administration, in the transfer with the aid of agrobacteria or in insertion via DNA or RNA viruses. Vectors comprise plasmids, phagemids, bacteriophages or viral genomes.

The nucleic acids coding for a tumor-associated antigen identified according to the present technology may be used for transfection of host cells. Nucleic acids here mean both recombinant DNA and RNA. Recombinant RNA may be prepared by in-vitro transcription of a DNA template. Furthermore, it may be modified by stabilizing sequences, capping and polyadenylation prior to application.

According to the present technology, the term "host cell" relates to any cell which can be transformed or transfected with an exogenous nucleic acid. The term "host cells" comprises according to the present technology prokaryotic (e.g. E. coli) or eukaryotic cells (e.g. dendritic cells, B cells, CHO cells, COS cells, K562 cells, yeast cells and insect cells). Particular preference is given to mammalian cells such as cells from humans, mice, hamsters, pigs, goats, primates. The cells may be derived from a multiplicity of tissue types and comprise primary cells and cell lines. Specific examples comprise keratinocytes, peripheral blood leukocytes, stem cells of the bone marrow and embryonic stem cells. In further embodiments, the host cell is an antigen-presenting cell, in particular a dendritic cell, monocyte or a macrophage. A nucleic acid may be present in the host cell in the form of a single copy or of two or more copies and, in one embodiment, is expressed in the host cell.

According to the present technology, the term "expression" is used in its most general meaning and comprises the production of RNA or of RNA and protein. It also comprises partial expression of nucleic acids. Furthermore, expression may be carried out transiently or stably. Preferred expression systems in mammalian cells comprise pcDNA3.1 and pRc/CMV (Invitrogen, Carlsbad, Calif.), which contain a selectable marker such as a gene imparting resistance to G418 (and thus enabling stably transfected cell lines to be selected) and the enhancer-promoter sequences of cytomegalovirus (CMV).

In those cases of the present technology in which a MHC molecule presents a tumor-associated antigen or a part thereof, an expression vector may also comprise a nucleic acid sequence coding for said MHC molecule. The nucleic acid sequence coding for the MHC molecule may be present on the same expression vector as the nucleic acid coding for the tumor-associated antigen or the part thereof, or both nucleic acids may be present on different expression vectors. In the latter case, the two expression vectors may be cotransfected into a cell. If a host cell expresses neither the tumor-

associated antigen or the part thereof nor the MHC molecule, both nucleic acids coding therefor may be transfected into the cell either on the same expression vector or on different expression vectors. If the cell already expresses the MHC molecule, only the nucleic acid sequence coding for the tumor-associated antigen or the part thereof can be transfected into the cell.

The present technology also comprises kits for detection and/or determination of the quantity of nucleic acids. Such kits comprise, for example, a pair of amplification primers which hybridize to the nucleic acid which is to be detected or the amount of which is to be determined. The primers preferably comprise a sequence of 6-50, in particular 10-30, 15-30 and 20-30 contiguous nucleotides of the nucleic acid and are nonoverlapping, in order to avoid the formation of primer dimers. One of the primers will hybridize to one strand of the nucleic acid, and the other primer will hybridize to the complementary strand in an arrangement which allows amplification of the nucleic acid.

"Antisense molecules" or "antisense nucleic acids" may be used for regulating, in particular reducing, expression of a nucleic acid. The term "antisense molecule" or "antisense nucleic acid" refers according to the present technology to an oligonucleotide which is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide or modified oligodeoxyribonucleotide and which hybridizes under physiological conditions to DNA comprising a particular gene or to mRNA of said gene, thereby inhibiting transcription of said gene and/or translation of said mRNA. According to the present technology, an "antisense molecule" also comprises a construct which contains a nucleic acid or a part thereof in reverse orientation with respect to its natural promoter. An antisense transcript of a nucleic acid or of a part thereof may form a duplex with naturally occurring mRNA and thus prevent accumulation of or translation of the mRNA. Another possibility is the use of ribozymes for inactivating a nucleic acid.

Antisense oligonucleotides preferred according to the present technology have a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of the target nucleic acid and preferably are fully complementary to the target nucleic acid or to a part thereof.

In preferred embodiments, the antisense oligonucleotide hybridizes with an N-terminal or 5' upstream site such as a translation initiation site, transcription initiation site or promoter site. In further embodiments, the antisense oligonucleotide hybridizes with a 3'untranslated region or mRNA splicing site.

In one embodiment, an oligonucleotide of the present technology consists of ribonucleotides, deoxyribonucleotides or a combination thereof, with the 5' end of one nucleotide and the 3' end of another nucleotide being linked to one another by a phosphodiester bond. These oligonucleotides may be synthesized in the conventional manner or produced recombinantly.

In preferred embodiments, an oligonucleotide of the present technology is a "modified" oligonucleotide. Here, the oligonucleotide may be modified in very different ways, without impairing its ability to bind its target, in order to increase, for example, its stability or therapeutic efficacy. According to the present technology, the term "modified oligonucleotide" means an oligonucleotide in which (i) at least two of its nucleotides are linked to one another by a synthetic internucleoside bond (i.e. an internucleoside bond which is not a phosphodiester bond) and/or (ii) a chemical group which is usually not found in nucleic acids is covalently linked to the oligonucleotide. Preferred synthetic internucleoside bonds are phosphorothioates, alkyl phosphonates,

phosphorodithioates, phosphate esters, alkyl phosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also comprises oligonucleotides having a covalently modified base and/or sugar. "Modified oligonucleotides" comprise, for example, oligonucleotides with sugar residues which are covalently bound to low molecular weight organic groups other than a hydroxyl group at the 3' position and a phosphate group at the 5' position. Modified oligonucleotides may comprise, for example, a 2'-O-alkylated ribose residue or another sugar instead of ribose, such as arabinose.

It is to be understood that all embodiments described above with respect to oligonucleotides may also apply to polynucleotides.

By "small interfering RNA" or "siRNA" as used herein is meant an isolated RNA molecule, preferably greater than 10 nucleotides in length, more preferably greater than 15 nucleotides in length, and most preferably 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length that is used to identify a target gene or mRNA to be degraded. A range of 19-25 nucleotides is the most preferred size for siRNAs.

siRNA according to the present technology can comprise partially purified RNA, substantially pure RNA, synthetic RNA, or recombinantly produced RNA, as well as altered RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siRNA or to one or more internal nucleotides of the siRNA; modifications that make the siRNA resistant to nuclease digestion (e. g., the use of 2'-substituted ribonucleotides or modifications to the sugar-phosphate backbone); or the substitution of one or more nucleotides in the siRNA with deoxyribonucleotides. Furthermore, siRNA may be modified to increase the stability thereof as described above for modified oligonucleotides, in particular by introducing one or more phosphorothioate linkages.

One or both strands of the siRNA can also comprise a 3'-overhang. As used herein, a "3'-overhang" refers to at least one unpaired nucleotide extending from the 3'-end of an RNA strand. Thus in one embodiment, the siRNA comprises at least one 3'-overhang of from 1 to about 6 nucleotides (which includes ribonucleotides or deoxynucleotides) in length, preferably from 1 to about 5 nucleotides in length, more preferably from 1 to about 4 nucleotides in length, and particularly preferably from about 2 to about 4 nucleotides in length. In the embodiment in which both strands of the siRNA molecule comprise a 3'-overhang, the length of the overhangs can be the same or different for each strand. In a most preferred embodiment, the 3'-overhang is present on both strands of the siRNA, and is 2 nucleotides in length. For example, each strand of the siRNA of the present technology can comprise 3'-overhangs of dideoxythymidylic acid ("TT") or diuridylic acid ("uu").

In order to enhance the stability of the siRNA, the 3'-overhangs can be also stabilized against degradation. In one embodiment, the overhangs are stabilized by including purine nucleotides, such as adenosine or guanosine nucleotides. Alternatively, substitution of pyrimidine nucleotides by modified analogues, e.g., substitution of uridine nucleotides in the 3'-overhangs with 2'-deoxythymidine, is tolerated and does not affect the efficiency of RNAi degradation. In particular, the absence of a 2'-hydroxyl in the 2'-deoxythymidine significantly enhances the nuclease resistance of the 3'-overhang in tissue culture medium.

The sense and antisense strands of the siRNA can comprise two complementary, single-stranded RNA molecules or can comprise a single molecule in which two complementary portions are base-paired and are covalently linked by a single-stranded "hairpin" area. That is, the sense region and anti-sense region can be covalently connected via a linker molecule. The linker molecule can be a polynucleotide or non-nucleotide linker. Without wishing to be bound by any theory, it is believed that the hairpin area of the latter type of siRNA molecule is cleaved intracellularly by the "Dicer" protein (or its equivalent) to form a siRNA of two individual base-paired RNA molecules.

As used herein, "target mRNA" refers to an RNA molecule that is a target for downregulation.

siRNA can be expressed from pol III expression vectors without a change in targeting site, as expression of RNAs from pol III promoters is only believed to be efficient when the first transcribed nucleotide is a purine.

siRNA according to the present technology can be targeted to any stretch of approximately 19-25 contiguous nucleotides in any of the target mRNA sequences (the "target sequence"). Techniques for selecting target sequences for siRNA are given, for example, in Tuschl T. et al., "The siRNA User Guide", revised Oct. 11, 2002, the entire disclosure of which is herein incorporated by reference. "The siRNA User Guide" is available on the world wide web at a website maintained by Dr. Thomas Tuschl, Laboratory of RNA Molecular Biology, Rockefeller University, New York, USA, and can be found by accessing the website of the Rockefeller University and searching with the keyword "siRNA". Thus, the sense strand of the present siRNA comprises a nucleotide sequence substantially identical to any contiguous stretch of about 19 to about 25 nucleotides in the target mRNA.

Generally, a target sequence on the target mRNA can be selected from a given cDNA sequence corresponding to the target mRNA, preferably beginning 50 to 100 nt downstream (i.e., in the 3'-direction) from the start codon. The target sequence can, however, be located in the 5'- or 3'-untranslated regions, or in the region nearby the start codon.

siRNA can be obtained using a number of techniques known to those of skill in the art. For example, siRNA can be chemically synthesized or recombinantly produced using methods known in the art, such as the Drosophila in vitro system described in U.S. published application 2002/0086356 of Tuschl et al., the entire disclosure of which is herein incorporated by reference.

Preferably, siRNA is chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. siRNA can be synthesized as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

Alternatively, siRNA can also be expressed from recombinant circular or linear DNA plasmids using any suitable promoter. Such embodiments are included according to the present technology when reference is made herein to the administration of siRNA or the incorporation of siRNA into pharmaceutical compositions. Suitable promoters for expressing siRNA of the present technology from a plasmid include, for example, the U6 or H1 RNA pol III promoter sequences and the cytomegalovirus promoter.

Selection of other suitable promoters is within the skill in the art. The recombinant plasmids of the present technology can also comprise inducible or regulatable promoters for expression of the siRNA in a particular tissue or in a particular intracellular environment.

The siRNA expressed from recombinant plasmids can either be isolated from cultured cell expression systems by

standard techniques, or can be expressed intracellularly. The use of recombinant plasmids to deliver siRNA to cells in vivo is discussed in more detail below. siRNA can be expressed from a recombinant plasmid either as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

Selection of plasmids suitable for expressing siRNA, methods for inserting nucleic acid sequences for expressing the siRNA into the plasmid, and methods of delivering the recombinant plasmid to the cells of interest are within the skill in the art.

siRNA can also be expressed from recombinant viral vectors intracellularly in vivo. The recombinant viral vectors comprise sequences encoding the siRNA and any suitable promoter for expressing the siRNA sequences. The recombinant viral vectors can also comprise inducible or regulatable promoters for expression of the siRNA in a particular tissue or in a particular intracellular environment. siRNA can be expressed from a recombinant viral vector either as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

The term "peptide" comprises oligo- and polypeptides and refers to substances comprising two or more, preferably 3 or more, preferably 4 or more, preferably 6 or more, preferably 8 or more, preferably 10 or more, preferably 13 or more, preferably 16 more, preferably 21 or more and up to preferably 8, 10, 20, 30, 40 or 50, in particular 100 amino acids joined covalently by peptide bonds. The term "protein" refers to large peptides, preferably to peptides with more than 100 amino acid residues, but in general the terms "peptides" and "proteins" are synonyms and are used interchangeably herein.

Preferably, the proteins and peptides described according to the present technology have been isolated. The terms "isolated protein" or "isolated peptide" mean that the protein or peptide has been separated from its natural environment. An isolated protein or peptide may be in an essentially purified state. The term "essentially purified" means that the protein or peptide is essentially free of other substances with which it is associated in nature or in vivo.

Such proteins and peptides may be used, for example, in producing antibodies and in an immunological or diagnostic assay or as therapeutics. Proteins and peptides described according to the present technology may be isolated from biological samples such as tissue or cell homogenates and may also be expressed recombinantly in a multiplicity of pro- or eukaryotic expression systems.

For the purposes of the present technology, "derivatives" of a protein or peptide or of an amino acid sequence comprise amino acid insertion variants, amino acid deletion variants and/or amino acid substitution variants.

Amino acid insertion variants comprise amino- and/or carboxy-terminal fusions and also insertions of single or two or more amino acids in a particular amino acid sequence. In the case of amino acid sequence variants having an insertion, one or more amino acid residues are inserted into a particular site in an amino acid sequence, although random insertion with appropriate screening of the resulting product is also possible.

Amino acid deletion variants are characterized by the removal of one or more amino acids from the sequence.

Amino acid substitution variants are characterized by at least one residue in the sequence being removed and another residue being inserted in its place. Preference is given to the modifications being in positions in the amino acid sequence which are not conserved between homologous proteins or peptides and/or to replacing amino acids with other ones having similar properties.

"Conservative substitutions" may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α-helices. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

Preferably the degree of similarity, preferably identity between a specific amino acid sequence described herein and an amino acid sequence which is a derivative of said specific amino acid sequence will be at least 70%, preferably at least 80%, preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%. The degree of similarity or identity is given preferably for a region of at least about 20, at least about 40, at least about 60, at least about 80, at least about 100, at least about 120, at least about 140, at least about 160, at least about 200 or 250 amino acids. In preferred embodiments, the degree of similarity or identity is given for the entire length of the reference amino acid sequence.

In one embodiment, a protein or peptide which is a derivative of a specific protein or peptide or which is a part of a specific protein or peptide has a relevant function and/or activity of the specific protein or peptide, i.e. it may have the same activity or immunological properties as the specific protein or peptide.

The amino acid variants described above may be readily prepared with the aid of known peptide synthesis techniques such as, for example, by solid phase synthesis (Merrifield, 1964) and similar methods or by recombinant DNA manipulation. The manipulation of DNA sequences for preparing proteins and peptides having substitutions, insertions or deletions, is described in detail in Sambrook et al. (1989), for example.

According to the present technology, "derivatives" of proteins and peptides also comprise single or multiple substitutions, deletions and/or additions of any molecules associated with the protein or peptide, such as carbohydrates, lipids and/or proteins or peptides. The term "derivative" also extends to all functional chemical equivalents of said proteins and peptides.

According to the present technology, a part or fragment of a tumor-associated antigen preferably has a functional property of the protein or peptide from which it has been derived. Such functional properties comprise the interaction with antibodies, the interaction with other peptides or proteins, the selective binding of nucleic acids and an enzymatic activity. A particular property is the ability to form a complex with MHC molecules and, where appropriate, generate an immune response, preferably by stimulating cytotoxic or T helper cells. A part or fragment of a tumor-associated antigen preferably comprises a sequence of at least 6, in particular at least 8, at least 10, at least 12, at least 15, at least 20, at least 30 or at least 50, consecutive amino acids of the tumor-associated antigen. A part or fragment of a tumor-associated antigen

preferably comprises a sequence of up to 8, in particular up to 10, up to 12, up to 15, up to 20, up to 30 or up to 55, consecutive amino acids of the tumor-associated antigen. A part or fragment of a tumor-associated antigen is preferably a part of the tumor-associated antigen which corresponds to the non-transmembrane portion, in particular the extracellular portion of the antigen, or is comprised thereof.

Preferred parts or fragments of a tumor-associated antigen are in particular suitable for the stimulation of cytotoxic T-lymphocytes in vivo but also for the production of expanded and stimulated T-lymphocytes for the therapeutic adoptive transfer ex vivo.

A part or a fragment of a nucleic acid coding for a tumor-associated antigen relates according to the present technology to the part of the nucleic acid, which codes at least for the tumor-associated antigen and/or for a part or a fragment of said tumor-associated antigen, as defined above. A part or fragment of a nucleic acid coding for a tumor-associated antigen is preferably that part of the nucleic acid corresponding to the open reading frame.

According to the present technology, particular embodiments ought to involve providing "dominant negative" proteins or peptides derived from tumor-associated antigens. A dominant negative protein or peptide is an inactive protein or peptide variant which, by way of interacting with the cellular machinery, displaces an active protein or peptide from its interaction with the cellular machinery or which competes with the active protein or peptide, thereby reducing the effect of said active protein.

Antisera which contain specific antibodies specifically binding to the target protein can be prepared by various standard processes; see, for example, "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane, ISBN: 0879693142 and "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN 0879695447. Thereby it is also possible to generate affine and specific antibodies which recognize complex membrane proteins in their native form (Azorsa et al., J. Immunol. Methods 229: 35-48, 1999; Anderson et al., J. Immunol. 143: 1899-1904, 1989; Gardsvoll, J. Immunol. Methods 234: 107-116, 2000). This is in particular relevant for the preparation of antibodies which are to be used therapeutically, but also for many diagnostic applications. In this respect, it is possible to immunize with the whole protein, with extracellular partial sequences as well as with cells which express the target molecule in physiologically folded form.

Monoclonal antibodies are traditionally prepared using the hybridoma technology. (for technical details see: "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142; "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447).

It is known that only a small part of an antibody molecule, the paratope, is involved in binding of the antibody to its epitope (cf. Clark, W. R. (1986), *The Experimental Foundations of Modern Immunology*, Wiley & Sons, Inc., New York; Roitt, I. (1991), *Essential Immunology*, 7th Edition, Blackwell Scientific Publications, Oxford). The pFc' and Fc regions are, for example, effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically removed or which has been produced without the pFc' region, referred to as F(ab')$_2$ fragment, carries both antigen binding sites of a complete

antibody. Similarly, an antibody from which the Fc region has been enzymatically removed or which has been produced without said Fc region, referred to as Fab fragment, carries one antigen binding site of an intact antibody molecule. Furthermore, Fab fragments consist of a covalently bound light chain of an antibody and part of the heavy chain of said antibody, referred to as Fd. The Fd fragments are the main determinants of antibody specificity (a single Fd fragment can be associated with up to ten different light chains, without altering the specificity of the antibody) and Fd fragments, when isolated, retain the ability to bind to an epitope.

Located within the antigen-binding part of an antibody are complementary-determining regions (CDRs) which interact directly with the antigen epitope and framework regions (FRs) which maintain the tertiary structure of the paratope. Both the Fd fragment of the heavy chain and the light chain of IgG immunoglobulins contain four framework regions (FR1 to FR4) which are separated in each case by three complementary-determining regions (CDR1 to CDR3). The CDRs and, in particular, the CDR3 regions and, still more particularly, the CDR3 region of the heavy chain are responsible to a large extent for antibody specificity.

Non-CDR regions of a mammalian antibody are known to be able to be replaced by similar regions of antibodies with the same or a different specificity, with the specificity for the epitope of the original antibody being retained. This made possible the development of "humanized" antibodies in which nonhuman CDRs are covalently linked to human FR and/or Fc/pFc' regions to produce a functional antibody.

As another example, WO 92/04381 describes the production and use of humanized murine RSV antibodies in which at least part of the murine FR regions have been replaced with FR regions of a human origin. Antibodies of this kind, including fragments of intact antibodies with antigen-binding capability, are often referred to as "chimeric" antibodies.

According to the present technology, the term "antibody" also includes F(ab')$_2$, Fab, Fv, and Fd fragments of antibodies, chimeric antibodies, in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman sequences, chimeric F(ab')$_2$-fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman sequences, chimeric Fab-fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman sequences, and chimeric Fd-fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced with homologous human or nonhuman sequences. The term "antibody" also comprises "single-chain" antibodies.

The present technology also comprises proteins and peptides which bind specifically to tumor-associated antigens. Binding substances of this kind may be provided, for example, by degenerate peptide libraries which may be prepared simply in solution in an immobilized form or as phage-display libraries. It is likewise possible to prepare combinatorial libraries of peptides with one or more amino acids. Libraries of peptoids and nonpeptidic synthetic residues may also be prepared.

Antibodies may also be coupled to specific diagnostic substances for displaying cells and tissues expressing tumor-associated antigens. They may also be coupled to therapeutically useful substances.

Diagnostic substances or agents include any label that functions to: (i) provide a detectable signal; (ii) interact with a second label to modify the detectable signal provided by the

first or second label, e.g. FRET (Fluorescence Resonance Energy Transfer); (iii) affect mobility, e.g. electrophoretic mobility, by charge, hydrophobicity, shape, or other physical parameters, or (iv) provide a capture moiety, e.g., affinity, antibody/antigen, or ionic complexation. Suitable as label are structures, such as fluorescent labels, luminescent labels, chromophore labels, radioisotopic labels, isotopic labels, preferably stable isotopic labels, isobaric labels, enzyme labels, particle labels, in particular metal particle labels, magnetic particle labels, polymer particle labels, small organic molecules such as biotin, ligands of receptors or binding molecules such as cell adhesion proteins or lectins, label-sequences comprising nucleic acids and/or amino acid residues which can be detected by use of binding agents, etc. Diagnostic substances comprise, in a nonlimiting manner, barium sulfate, iocetamic acid, iopanoic acid, calcium ipodate, sodium diatrizoate, meglumine diatrizoate, metrizamide, sodium tyropanoate and radio diagnostic, including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance, such as fluorine and gadolinium.

According to the present technology, the terms "therapeutically useful substance", "therapeutic substance" or "therapeutic agent" means any molecule which may exert a therapeutic effect. According to the present technology, a therapeutically useful substance is preferably selectively guided to a cell which expresses one or more tumor-associated antigens and includes anticancer agents, radioactive iodine-labeled compounds, toxins, cytostatic or cytolytic drugs, etc. Anticancer agents comprise, for example, aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubin, doxorubicin, taxol, etoposide, fluorouracil, interferon-α, lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Other anticancer agents are described, for example, in Goodman and Gilman, "The Pharmacological Basis of Therapeutics", 8th Edition, 1990, McGraw-Hill, Inc., in particular Chapter 52 (Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner). Toxins may be proteins such as pokeweed antiviral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin or *Pseudomonas* exotoxin. Toxin residues may also be high energy-emitting radionuclides such as cobalt-60.

The term "major histocompatibility complex" or "MHC" relates to a complex of genes present in all vertebrates. MHC proteins or molecules are involved in signaling between lymphocytes and antigen presenting cells in normal immune reactions by binding peptides and presenting them for recognition by T cell receptors (TCR). MHC molecules bind peptides within an intracellular processing compartment and present these peptides on the surface of antigen presenting cells for recognition by T cells. The human MHC region also termed HLA is located on chromosome 6 and includes the class I and class II region. In one preferred embodiment of all aspects of the present technology an MHC molecule is an HLA molecule.

"Reduce" or "inhibit" as used herein means the ability to cause an overall decrease, preferably of 20% or greater, more preferably of 50% or greater, and most preferably of 75% or greater, in the level, e.g. in the level of protein or mRNA as compared to a reference sample (e.g., a sample not treated with siRNA). This reduction or inhibition of RNA or protein expression can occur through targeted mRNA cleavage or degradation. Assays for protein expression or nucleic acid

expression are known in the art and include, for example, ELISA, western blot analysis for protein expression, and northern blotting or RNase protection assays for RNA.

The term "patient" means according to the present technology a human being, a nonhuman primate or another animal, in particular a mammal such as a cow, horse, pig, sheep, goat, dog, cat or a rodent such as a mouse and rat. In a particularly preferred embodiment, the patient is a human being.

According to the present technology the term "increased" or "increased amount" preferably refers to an increase by at least 10%, in particular at least 20%, at least 50% or at least 100%. The amount of a substance is also increased in a test sample such as a biological sample compared to a reference sample if it is detectable in the test sample but absent or not detectable in the reference sample.

According to the present technology, the term "disease" refers to any pathological state in which tumor-associated nucleic acids and/or tumor-associated antigens are expressed or abnormally expressed. "Abnormal expression" means according to the present technology that expression is altered, preferably increased, compared to the state in a healthy individual. An increase in expression refers to an increase by at least 10%, in particular at least 20%, at least 50% or at least 100%. In one embodiment, expression is only found in tissue of a diseased individual, while expression in a healthy individual is repressed or is repressed in a healthy individual except for placenta. One example of such a disease is cancer, wherein the term "cancer" according to the present technology comprises leukemias, seminomas, melanomas, teratomas, lymphomas, neuroblastomas, gliomas, rectal cancer, endometrial cancer, kidney cancer, adrenal cancer, thyroid cancer, blood cancer, skin cancer, cancer of the brain, cervical cancer, intestinal cancer, liver cancer, colon cancer, stomach cancer, intestine cancer, head and neck cancer, gastrointestinal cancer, lymph node cancer, esophagus cancer, colorectal cancer, pancreas cancer, ear, nose and throat (ENT) cancer, breast cancer, prostate cancer, cancer of the uterus, ovarian cancer and lung cancer and the matastases thereof. Examples thereof are lung carcinomas, mamma carcinomas, prostate carcinomas, colon carcinomas, renal cell carcinomas, cervical carcinomas, or metastases of the cancer types or tumors described above. The term cancer according to the present technology also comprises cancer metastases.

By "tumor" is meant an abnormal group of cells or tissue that grows by a rapid, uncontrolled cellular proliferation and continues to grow after the stimuli that initiated the new growth cease. Tumors show partial or complete lack of structural organization and functional coordination with the normal tissue, and usually form a distinct mass of tissue, which may be either benign or malignant.

By "metastasis" is meant the spread of cancer cells from its original site to another part of the body. The formation of metastasis is a very complex process and depends on detachment of malignant cells from the primary tumor, invasion of the extracellular matrix, penetration of the endothelial basement membranes to enter the body cavity and vessels, and then, after being transported by the blood, infiltration of target organs. Finally, the growth of a new tumor at the target site depends on angiogenesis. Tumor metastasis often occurs even after the removal of the primary tumor because tumor cells or components may remain and develop metastatic potential. In one embodiment, the term "metastasis" according to the present technology relates to "distant metastasis" which relates to a metastasis which is remote from the primary tumor and the regional lymph node system.

According to the present technology, a biological sample may be a tissue sample, including bodily fluids, and/or a cellular sample and may be obtained in the conventional manner such as by tissue biopsy, including punch biopsy, and by taking blood, bronchial aspirate, sputum, urine, feces or other body fluids. According to the present technology, the term "biological sample" also includes fractions of biological samples. Preferably, the term "biological sample" according to the present technology does not include samples derived from placental tissue.

According to the present technology, the term "immunoreactive cell" means a cell which can mature into an immune cell (such as B cell, T helper cell, or cytolytic T cell) with suitable stimulation. Immunoreactive cells comprise CD34$^+$ hematopoietic stem cells, immature and mature T cells and immature and mature B cells. If production of cytolytic or T helper cells recognizing a tumor-associated antigen is desired, the immunoreactive cell is contacted with a cell expressing a tumor-associated antigen under conditions which favor production, differentiation and/or selection of cytolytic T cells and of T helper cells. The differentiation of T cell precursors into a cytolytic T cell, when exposed to an antigen, is similar to clonal selection of the immune system.

The terms "T cell" and "T lymphocyte" are used interchangeably herein and include T helper cells and cytotoxic T cells which comprise cytolytic T cells.

Some therapeutic methods are based on a reaction of the immune system of a patient, which results in a lysis of antigen-presenting cells such as cancer cells which present one or more tumor-associated antigens. In this connection, for example autologous cytotoxic T lymphocytes specific for a complex of a tumor-associated antigen and an MHC molecule are administered to a patient having a cellular abnormality. The production of such cytotoxic T lymphocytes in vitro is known. An example of a method of differentiating T cells can be found in WO-A-9633265. Generally, a sample containing cells such as blood cells is taken from the patient and the cells are contacted with a cell which presents the complex and which can cause propagation of cytotoxic T lymphocytes (e.g. dendritic cells). The target cell may be a transfected cell such as a COS cell. These transfected cells present the desired complex on their surface and, when contacted with cytotoxic T lymphocytes, stimulate propagation of the latter. The clonally expanded autologous cytotoxic T lymphocytes are then administered to the patient.

In another method of selecting antigen-specific cytotoxic T lymphocytes, fluorogenic tetramers of MHC class I molecule/peptide complexes are used for obtaining specific clones of cytotoxic T lymphocytes (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998).

The present technology also includes therapeutic methods referred to as adoptive transfer (Greenberg, *J. Immunol.* 136 (5):1917, 1986; Riddel et al., *Science* 257:238, 1992; Lynch et al., *Eur. J. Immunol.* 21:1403-1410, 1991; Kast et al., *Cell* 59:603-614, 1989), wherein cells presenting the desired complex (e.g. dendritic cells) are combined with cytotoxic T lymphocytes of the patient to be treated, resulting in a propagation of specific cytotoxic T lymphocytes. The propagated cytotoxic T lymphocytes are then administered to a patient having a cellular anomaly characterized by particular abnormal cells presenting the specific complex. The cytotoxic T lymphocytes then lyse the abnormal cells, thereby achieving a desired therapeutic effect.

Furthermore, cells presenting the desired complex (e.g. dendritic cells) may be combined with cytotoxic T lymphocytes of healthy individuals or another species (e.g. mouse) which may result in propagation of specific cytotoxic T lym-

phocytes with high affinity. The high affinity T cell receptor of these propagated specific T lymphocytes may be cloned and optionally humanized to a different extent, and the T cell receptors thus obtained then transduced via gene transfer, for example using retroviral vectors, into T cells of patients. Adoptive transfer may then be carried out using these genetically altered T lymphocytes (Stanislawski et al., Nat Immunol. 2:962-70, 2001; Kessels et al., Nat Immunol. 2:957-61, 2001).

Adoptive transfer is not the only form of therapy which can be applied according to the present technology. Cytotoxic T lymphocytes may also be generated in vivo in a manner known per se. One method uses nonproliferative cells expressing the complex. The cells used here will be those which usually express the complex, such as irradiated tumor cells or cells transfected with one or both genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting MHC molecule). Another preferred form is the introduction of the tumor-associated antigen in the form of recombinant RNA which may be introduced into cells by liposomal transfer or by electroporation, for example. The resulting cells present the complex of interest and are recognized by autologous cytotoxic T lymphocytes which then propagate.

A similar effect can be achieved by combining the tumor-associated antigen or a fragment thereof with an adjuvant in order to make incorporation into antigen-presenting cells in vivo possible. The tumor-associated antigen or a fragment thereof may be represented as protein, as DNA (e.g. within a vector) or as RNA. The tumor-associated antigen is processed to produce a peptide partner for the MHC molecule, while a fragment thereof may be presented without the need for further processing. The latter is the case in particular, if these can bind to MHC molecules. Preference is given to administration forms in which the complete antigen is processed in vivo by a dendritic cell, since this may also produce T helper cell responses which are needed for an effective immune response (Ossendorp et al., *Immunol Lett.* 74:75-9, 2000; Ossendorp et al., *J. Exp. Med.* 187:693-702, 1998). In general, it is possible to administer an effective amount of the tumor-associated antigen to a patient by intradermal injection, for example. However, injection may also be carried out intranodally into a lymph node (Maloy et al., *Proc Natl Acad Sci USA* 98:3299-303, 2001).

The pharmaceutical compositions and methods of treatment described according to the present technology may also be used for immunization or vaccination to therapeutically treat or prevent a disease described herein. According to the present technology, the terms "immunization" or "vaccination" preferably relate to an increase in or activation of an immune response to an antigen. It is possible to use animal models for testing an immunizing effect on cancer by using a tumor-associated antigen or a nucleic acid coding therefor. For example, human cancer cells may be introduced into a mouse to generate a tumor, and one or more nucleic acids coding for tumor-associated antigens may be administered. The effect on the cancer cells (for example reduction in tumor size) may be measured as a measure for the effectiveness of an immunization by the nucleic acid.

As part of the composition for an immunization or a vaccination, preferably one or more tumor-associated antigens or stimulating fragments thereof are administered together with one or more adjuvants for inducing an immune response or for increasing an immune response. An adjuvant is a substance which is incorporated into the antigen or administered together with the latter and which enhances the immune response. Adjuvants may enhance the immune response by providing an antigen reservoir (extracellularly or in macrophages), activating macrophages and/or stimulating particular lymphocytes. Adjuvants are known and comprise in a non-limiting way monophosphoryl lipid A (MPL, SmithKline Beecham), saponins such as QS21 (SmithKline Beecham), DQS21 (SmithKline Beecham; WO 96/33739), QS7, QS17, QS18 and QS-L1 (So et al., Mol. Cells 7:178-186, 1997), incomplete Freund's adjuvant, complete Freund's adjuvant, vitamin E, montanide, alum, CpG oligonucleotides (cf. Kreig et al., Nature 374:546-9, 1995) and various water-in-oil emulsions prepared from biologically degradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered in a mixture with DQS21/MPL. The ratio of DQS21 to MPL is typically about 1:10 to 10:1, preferably about 1:5 to 5:1 and in particular about 1:1. For administration to humans, a vaccine formulation typically contains DQS21 and MPL in a range from about 1 μg to about 100 μg.

Other substances which stimulate an immune response of the patient may also be administered. It is possible, for example, to use cytokines in a vaccination, owing to their regulatory properties on lymphocytes. Such cytokines comprise, for example, interleukin-12 (IL-12) which was shown to increase the protective actions of vaccines (cf. *Science* 268:1432-1434, 1995), GM-CSF and IL-18.

There are a number of compounds which enhance an immune response and which therefore may be used in a vaccination. Said compounds comprise costimulating molecules provided in the form of proteins or nucleic acids such as B7-1 and B7-2 (CD80 and CD86, respectively).

The present technology also provides for administration of nucleic acids, proteins or peptides. Proteins and peptides may be administered in a manner known per se. In one embodiment, nucleic acids are administered by ex vivo methods, i.e. by removing cells from a patient, genetic modification of said cells in order to incorporate a tumor-associated antigen and reintroduction of the altered cells into the patient. This generally comprises introducing a functional copy of a gene into the cells of a patient in vitro and reintroducing the genetically altered cells into the patient. The functional copy of the gene is under the functional control of regulatory elements which allow the gene to be expressed in the genetically altered cells. Transfection and transduction methods are known to the skilled worker. The present technology also provides for administering nucleic acids in vivo by using vectors such as viruses and target-controlled liposomes. If according to the present technology reference is made to the administration or incorporation into pharmaceutical compositions of nucleic acids this includes embodiments wherein the nucleic acid is present in such vectors.

In a preferred embodiment, a virus or viral vector for administering a nucleic acid coding for a tumor-associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, pox viruses, including vaccinia virus and attenuated pox viruses, Semliki Forest virus, retroviruses, Sindbis virus and Ty virus-like particles. Particular preference is given to adenoviruses and retroviruses. The retroviruses are typically replication-deficient (i.e. they are incapable of generating infectious particles).

Methods of introducing nucleic acids into cells in vitro or in vivo comprise transfection of nucleic acid calcium phosphate precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the above viruses carrying the nucleic acids of interest, liposome-mediated transfection, and the like. In particular embodiments, preference is given to directing the nucleic acid to particular cells. In such embodiments, a carrier used for administering a nucleic acid to a cell (e.g. a retrovirus or a liposome) may have a

bound target control molecule. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell may be incorporated into or attached to the nucleic acid carrier. Preferred antibodies comprise antibodies which bind selectively a tumor-associated antigen. If administration of a nucleic acid via liposomes is desired, proteins binding to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation in order to make target control and/or uptake possible. Such proteins comprise capsid proteins or fragments thereof which are specific for a particular cell type, antibodies to proteins which are internalized, proteins addressing an intracellular site, and the like.

The therapeutic compositions of the present technology may be administered in pharmaceutically compatible preparations. Such preparations may usually contain pharmaceutically compatible concentrations of salts, buffer substances, preservatives, carriers, supplementing immunity-enhancing substances such as adjuvants, e.g. CpG oligonucleotides, cytokines, chemokines, saponin, GM-CSF and/or RNA and, where appropriate, other therapeutically active compounds.

The therapeutically active compounds of the present technology may be administered via any conventional route, including by injection or infusion. The administration may be carried out, for example, orally, intravenously, intraperitoneally, intramuscularly, subcutaneously or transdermally. Preferably, antibodies are therapeutically administered by way of a lung aerosol. Antisense nucleic acids are preferably administered by slow intravenous administration.

The compositions of the present technology are administered in effective amounts. An "effective amount" refers to the amount which achieves a desired reaction or a desired effect alone or together with further doses. In the case of treatment of a particular disease or of a particular condition characterized by expression of one or more tumor-associated antigens, the desired reaction preferably relates to inhibition of the course of the disease. This comprises slowing down the progress of the disease and, in particular, interrupting or reversing the progress of the disease. The desired reaction in a treatment of a disease or of a condition may also be delay of the onset or a prevention of the onset of said disease or said condition. According to the present technology, a diagnosis or treatment of cancer may also include the diagnosis or treatment of cancer metastases which have already formed or will form. According to the present technology, the term "treatment" comprises therapeutic and prophylactic treatment, i.e. prevention.

An effective amount of a composition of the present technology will depend on the condition to be treated, the severeness of the disease, the individual parameters of the patient, including age, physiological condition, size and weight, the duration of treatment, the type of an accompanying therapy (if present), the specific route of administration and similar factors.

The pharmaceutical compositions of the present technology are preferably sterile and contain an effective amount of the therapeutically active substance to generate the desired reaction or the desired effect.

The doses administered of the compositions of the present technology may depend on various parameters such as the type of administration, the condition of the patient, the desired period of administration, etc. In the case that a reaction in a patient is insufficient with an initial dose, higher doses (or effectively higher doses achieved by a different, more localized route of administration) may be used.

Generally, doses of the tumor-associated antigen of from 1 ng to 1 mg, preferably from 10 ng to 100 µg, are formulated and administered for a treatment or for generating or increasing an immune response. If the administration of nucleic acids (DNA and RNA) coding for tumor-associated antigens is desired, doses of from 1 ng to 0.1 mg are formulated and administered.

The pharmaceutical compositions of the present technology are generally administered in pharmaceutically compatible amounts and in pharmaceutically compatible compositions. The term "pharmaceutically compatible" refers to a nontoxic material which does not interact with the action of the active component of the pharmaceutical composition. Preparations of this kind may usually contain salts, buffer substances, preservatives, carriers and, where appropriate, other therapeutically active compounds. When used in medicine, the salts should be pharmaceutically compatible. However, salts which are not pharmaceutically compatible may used for preparing pharmaceutically compatible salts and are included in the present technology. Pharmacologically and pharmaceutically compatible salts of this kind comprise in a nonlimiting way those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic acids, and the like. Pharmaceutically compatible salts may also be prepared as alkali metal salts or alkaline earth metal salts, such as sodium salts, potassium salts or calcium salts.

A pharmaceutical composition of the present technology may comprise a pharmaceutically compatible carrier. According to the present technology, the term "pharmaceutically compatible carrier" refers to one or more compatible solid or liquid fillers, diluents or encapsulating substances, which are suitable for administration to humans. The term "carrier" refers to an organic or inorganic component, of a natural or synthetic nature, in which the active component is combined in order to facilitate application. The components of the pharmaceutical composition of the present technology are usually such that no interaction occurs which substantially impairs the desired pharmaceutical efficacy.

The pharmaceutical compositions of the present technology may contain suitable buffer substances such as acetic acid in a salt, citric acid in a salt, boric acid in a salt and phosphoric acid in a salt.

The pharmaceutical compositions may, where appropriate, also contain suitable preservatives such as benzalkonium chloride, chlorobutanol, paraben and thimerosal.

The pharmaceutical compositions are usually provided in a uniform dosage form and may be prepared in a manner known per se. Pharmaceutical compositions of the present technology may be in the form of capsules, tablets, lozenges, solutions, suspensions, syrups, elixirs or in the form of an emulsion, for example.

Compositions suitable for parenteral administration usually comprise a sterile aqueous or nonaqueous preparation of the active compound, which is preferably isotonic to the blood of the recipient. Examples of compatible carriers and solvents are Ringer solution and isotonic sodium chloride solution. In addition, usually sterile, fixed oils are used as solution or suspension medium.

The present technology is described in detail by the figures and examples below, which are used only for illustration purposes and are not meant to be limiting. Owing to the description and the examples, further embodiments which are likewise included in the present technology are accessible to the skilled worker.

EXAMPLES

The techniques and methods mentioned herein are carried out in a manner known per se and are described, for example,

in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. All methods including the use of kits and reagents are carried out according to the manufacturers' information unless specifically indicated.

Example 1

Screening for Placenta-Specific Genes Aberrantly Activated in Tumors

Tissues and Cell Lines

Tissues were obtained as human surplus materials during routine diagnostic or therapeutic procedures and were stored at −80° C. until use. Cell lines were purchased from the American Type Culture Collection (ATCC) and the German Resource Collection of Microorganisms and Cell Culture (DSMZ).

RNA Isolation and Microarray Hybridization

Total RNA was isolated using the RNeasy Mini Kit protocol (Qiagen). Quantification of isolated RNA was performed using UV-spectroscopy and the quality was determined both by A_{260}/A_{280} ratio and Agilent bioanalyzer (Agilent Technologies). Five micrograms total RNA were used for cDNA synthesis with 5 pmol μl^{-1} T7-oligo(dT)$_{24}$ primer and was performed at 43° C. for 90 minutes with the "Superscript First-Strand Synthesis-System" for RT-PCR (Invitrogen). Second-strand synthesis was performed with complete cDNA. The cDNA solution was incubated at 16° C. for 2 hours followed by an incubation step for 20 min with 6 U T4-DNA polymerase at 16° C. and the reaction was stopped using 10 µl of 0.5 M EDTA. After purification of the double stranded cDNA using the GeneChip Sample Cleanup Module (Affymetrix) labeled cRNA was generated from the cDNA sample by an in vitro transcription reaction that was supplemented with biotin-11-CTP and biotin-16-UTP (Enzo Diagnostics) according to the manufacturer's instructions. The cRNA was quantified by A_{260}, and the quality was determined using the labchip bioanalyzer (Agilent). Only cRNA specimens with a high quality were selected for further analyses. Fragmented cRNA (15 µg) was used to prepare 300 µl hybridization cocktail (100 mM MES, 1 M NaCl, 20 mM EDTA, 0.01% Tween-20) containing 0.1 mg ml^{-1} of herring sperm DNA, and 0.5 mg ml^{-1} acetylated bovine serum albumin. Control cRNA was used in order to compare hybridization efficiencies between arrays and to standardize the quantification of measured transcript levels and was included as component of the 'Eukaryotic Hybridization Control kit' (Affymetrix, Santa Clara, Calif., USA). The cocktails were heated to 95° C. for 5 minutes, equilibrated at 45° C. for 5 minutes, and clarified by centrifugation. The cocktail was hybridized to HG U133 Plus 2.0 arrays (Affymetrix) at 45° C. for 16 hours. The arrays were washed and stained with a streptavidin-conjugated fluor using the GeneChip fluidics station protocol EukGE-WS2 (Affymetrix) according to the manufacturer's instructions. Arrays were scanned with an argon-ion laser confocal scanner (Hewlett-Packard, Santa Clara, Calif.) with detection at 570 nm. Data were extracted using Microarray Suite version 5.0 (Affymetrix) and linearly scaled to achieve an average intensity of 2,500 per gene. Text files were exported to determine the intensity of each interrogating oligonucleotide perfect match probe cells or mismatch probe cells. In addition, the ratios of 5'- and 3'-ends of mRNA were analyzed of six randomly selected specimens (two of each group) using microarray test-chips (Test3 Array) containing 24 human housekeeping/maintenance genes (Affymetrix) and RNA degradation was not observed.

Bioinformatic Analysis

The GeneChip® Operating Software 1.4 (Affymetrix) and ArrayAssist software package 5.2 (Stratagene) were used for statistical analyses.

Results

Screening of samples from the 18 normal tissues shown below in table 1 and 30 tumor cell lines of different entities shown below in table 2 resulted in the sequences described herein which are expressed in placenta among the normal tissues investigated and in tumor cell lines.

TABLE 1

Tissues used for microarray expression analysis	
Tissue	Number
Placenta	2
Testis	2
Mammary gland	2
Thymus	2
Skin	2
Liver	2
Colon	2
Esophagus	2
Stomach	2
Lung	2
Kidney	2
Lymph node	2
Skeletal muscle	2
Myocard	1
Brain	1
Cerebellum	1
resting PBMCs	2
activ. PBMCs	2

TABLE 2

Cell lines used for microarray expression analysis	
Cell line	Tissue
BT-549	Breast cancer
MDA-MB-231 metastasizing	Breast cancer
MDA-MB-231 non-metastasizing	Breast cancer
MDA-MB-435S	Breast cancer
MDA-MB-468	Breast cancer
SK-BR-3	Breast cancer
Caov-3	Ovarian cancer
FU-OV	Ovarian cancer
NIH-OVCAR-3	Ovarian cancer
COLO-205	Colorectal cancer
HCT-116	Colorectal cancer
HCT-116 DKO	Colorectal cancer
HCT-15	Colorectal cancer
HT-29	Colorectal cancer
LOVO	Colorectal cancer
SW-480	Colorectal cancer
CPC-N	Lung cancer
LOU-NH-91	Lung cancer
SHP-77	Lung cancer
SK-MES-1	Lung cancer
NCI-H-187	Lung cancer
NCI-H-209	Lung cancer
NCI-H-522	Lung cancer
DU-145	Prostate cancer
Uncap	Prostate cancer
PC-3	Prostate cancer
MEL-JUSO	Melanoma
Murkowski	Melanoma
SK-MEL-37	Melanoma
HELA	Cervical cancer

Example 2

Validation of the Identified Tumor-Associated Markers

1. Examination of RNA Expression

The identified tumor-associated markers are first validated with the aid of RNA which is obtained from various tissues or from tissue-specific cell lines. Since the differential expression pattern of healthy tissue in comparison with tumor tissue is of decisive importance for the subsequent therapeutic application, the target genes are preferably characterized with the aid of these tissue samples.

Total RNA is isolated from native tissue samples or from tumor cell lines by standard methods of molecular biology. Said isolation may be carried out, for example, with the aid of the RNeasy Maxi kit (Qiagen, Cat. No. 75162) according to the manufacturer's instructions. This isolation method is based on the use of chaotropic reagent guanidinium isothiocyanate. Alternatively, acidic phenol can be used for isolation (Chomczynski & Sacchi, Anal. Biochem. 162: 156-159, 1987). After the tissue has been worked up by means of guanidinium isothiocyanate, RNA is extracted with acidic phenol, subsequently precipitated with isopropanol and taken up in DEPC-treated water.

2-4 μg of the RNA isolated in this way are subsequently transcribed into cDNA, for example by means of Superscript II (Invitrogen) according to the manufacturer's protocol. cDNA synthesis is primed with the aid of random hexamers (e.g. Roche Diagnostics) according to standard protocols of the relevant manufacturer. For quality control, the cDNAs are amplified over 30 cycles, using primers specific for the p53 gene which is expressed only lowly. Only p53-positive cDNA samples will be used for the subsequent reaction steps.

The targets are analyzed in detail by carrying out an expression analysis by means of PCR or quantitative PCR (qPCR) on the basis of a cDNA archive which has been isolated from various normal and tumor tissues and from tumor cell lines. For this purpose, 0.5 μl of cDNA of the above reaction mixture is amplified by a DNA polymerase (e.g. 1 U of HotStar-Taq DNA polymerase, Qiagen) according to the protocols of the particular manufacturer (total volume of the reaction mixture: 25-50 μl). Aside from said polymerase, the amplification mixture comprises 0.3 mM dNTPs, reaction buffer (final concentration 1×, depending on the manufacturer of the DNA polymerase) and in each case 0.3 mM gene-specific "sense" and "antisense" primers.

The specific primers of the target gene are, as far as possible, selected in such a way that they are located in two different exons so that genomic contaminations do not lead to false-positive results. In a non-quantitative end point PCR, the cDNA is typically incubated at 95° C. for 15 minutes in order to denature the DNA and to activate the Hot-Start enzyme. Subsequently the DNA is amplified over 35 cycles (1 min at 95° C., 1 min at the primer-specific hybridization temperature (approx. 55-65° C.), 1 min at 72° C. to elongate the amplicons). Subsequently, 10 μl of the PCR mixture are applied to agarose gels and fractionated in the electric field. The DNA is made visible in the gels by staining with ethidium bromide and the PCR result is documented by way of a photograph.

As an alternative to conventional PCR, expression of a target gene may also be analyzed by quantitative real time PCR. Meanwhile various analytical systems are available for this analysis, of which the best known ones are the ABI PRISM sequence detection system (TaqMan, Applied Biosystems), the iCycler (Biorad) and the Light cycler (Roche

Diagnostics). As described above, a specific PCR mixture is subjected to a run in the real time instruments. By adding a DNA-intercalating dye (e.g. ethidium bromide, CybrGreen), the newly synthesized DNA is made visible by specific light excitation (according to the dye manufacturers' information). A multiplicity of points measured during amplification enables the entire process to be monitored and the nucleic acid concentration of the target gene to be determined quantitatively. The PCR mixture is normalized by measuring a housekeeping gene (e.g. 18S RNA, β-actin). Alternative strategies via fluorescently labeled DNA probes likewise allow quantitative determination of the target gene of a specific tissue sample (see TaqMan applications from Applied Biosystems).

As shown in FIG. 1, placenta was confirmed in RT-PCR analyses as the only healthy tissue expressing the nucleic acid sequence according to SEQ ID NO:540. No significant expression was found in any other normal tissue. However, high and significant levels of expression were found in breast cancer.

Quantitative real-time RT-PCR analyses revealed that the nucleic acid sequence according to SEQ ID NO:540 was expressed in significant levels in the majority of breast cancer samples analyzed; cf. FIG. 2.

2. Cloning

The complete target gene which is required for further characterization of the tumor-associated marker is cloned according to common molecular-biological methods (e.g. in "Current Protocols in Molecular Biology", John Wiley & Sons Ltd., Wiley InterScience). In order to clone the target gene or to analyze its sequence, said gene is first amplified by a DNA polymerase having a proof reading function (e.g. pfu, Roche Diagnostics). The amplicon is then ligated by standard methods into a cloning vector. Positive clones are identified by sequence analysis and subsequently characterized with the aid of prediction programs and known algorithms.

3. Prediction of the Protein

Genes found according to the present technology (in particular those from the RefSeq XM domain) may require cloning of the full-length gene, determination of the open reading frame and deduction and analysis of the protein sequence.

In order to clone the full-length sequence, common protocols for the rapid amplification of cDNA ends and the screening of cDNA expression libraries with gene-specific probes may be used (Sambrook et al., *Molecular Cloning: A Laboratory Manual,* 2nd edition (1989), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

After assembling the fragments found in this way, potential open reading frames (ORF) can be predicted using common prediction programs. Since the position of the PolyA tail and of polyadenylation motifs predetermines the orientation of the potential gene product, only the 3 reading frames of that particular orientation remain out of a possible 6 reading frames. The former often yield only one sufficiently large open reading frame which may code for a protein, while the other reading frames have too many stop codons and would not code for any realistic protein. In the case of alternative open reading frames, identification of the authentic ORF is assisted by taking into account the Kozak criteria for optimal transcription initiation and by analyzing the deduced protein sequences which may arise. Said ORF is further verified by generating immune sera against proteins deduced from the potential ORFs and analyzing said immune sera for recognition of a real protein in tissues and cell lines.

4. Production of Antibodies

The tumor-associated antigens identified according to the present technology are characterized, for example, by using

antibodies. The present technology further comprises the diagnostic or therapeutic use of antibodies. Antibodies may recognize proteins in the native and/or denatured state (Anderson et al., *J. Immunol.* 143: 1899-1904, 1989; Gardsvoll, *J. Immunol. Methods* 234: 107-116, 2000; Kayyem et al., *Eur. J. Biochem.* 208: 1-8, 1992; Spiller et al., *J. Immunol. Methods* 224: 51-60, 1999).

Antisera comprising specific antibodies which specifically bind to the target protein may be prepared by various standard methods; cf., for example, "Monoclonal Antibodies: A Practical Approach" by Phillip Shepherd, Christopher Dean ISBN 0-19-963722-9, "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142 and "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447. It is also possible here to generate affine and specific antibodies which recognize complex membrane proteins in their native form (Azorsa et al., *J. Immunol. Methods* 229: 35-48, 1999; Anderson et al., *J. Immunol.* 143: 1899-1904, 1989; Gardsvoll, *J. Immunol. Methods.* 234: 107-116, 2000). This is especially important in the preparation of antibodies which are intended to be used therapeutically but also for many diagnostic applications. For this purpose, both the complete protein and extracellular partial sequences may be used for immunization.

Immunization and Production of Polyclonal Antibodies

Various immunization protocols are published. A species (e.g. rabbits, mice) is immunized by a first injection of the desired target protein. The immune response of the animal to the immunogen can be enhanced by a second or third immunization within a defined period of time (approx. 2-4 weeks after the previous immunization). Blood is taken from said animals and immune sera obtained, again after various defined time intervals (1st bleeding after 4 weeks, then every 2-3 weeks, up to 5 takings). The immune sera taken in this way comprise polyclonal antibodies which may be used to detect and characterize the target protein in Western blotting, by flow cytometry, immunofluorescence or immunohistochemistry.

The animals are usually immunized by any of four well-established methods, with other methods also in existence. The immunization may be carried out using peptides specific for the target protein, using the complete protein, or using extracellular partial sequences of a protein which can be identified experimentally or via prediction programs. Since the prediction programs do not always work perfectly, it is also possible to employ two domains separated from one another by a transmembrane domain. In this case, one of the two domains has to be extracellular, which may then be proved experimentally (see below). Immunization is offered commercially by different service providers.

(1) In the first case, peptides (length: 8-12 amino acids) are synthesized by in vitro methods (possibly carried out by a commercial service), and said peptides are used for immunization. Normally 3 immunizations are carried out (e.g. with a concentration of 5-100 µg/immunization).

(2) Alternatively, immunization may be carried out using recombinant proteins. For this purpose, the cloned DNA of the target gene is cloned into an expression vector and the target protein is synthesized, for example, cell-free in vitro, in bacteria (e.g. *E. coli*), in yeast (e.g. *S. pombe*), in insect cells or in mammalian cells, according to the conditions of the particular manufacturer (e.g. Roche Diagnostics, Invitrogen, Clontech, Qiagen). It is also possible to synthesize the target protein with the aid of viral expression systems (e.g. baculovirus, vacciniavi-

rus, adenovirus). After it has been synthesized in one of said systems, the target protein is purified, normally by employing chromatographic methods. In this context, it is also possible to use for immunization proteins which have a molecular anchor as an aid for purification (e.g. His tag, Qiagen; FLAG tag, Roche Diagnostics; GST fusion proteins). A multiplicity of protocols can be found, for example, in "Current Protocols in Molecular Biology", John Wiley & Sons Ltd., Wiley InterScience. After the target protein has been purified, an immunization is carried out as described above.

(3) If a cell line is available which synthesizes the desired protein endogenously, it is also possible to use this cell line directly for preparing the specific antiserum. In this case, immunization is carried out by 1-3 injections with in each case approx. $1-5×10^7$ cells.

(4) The immunization may also be carried out by injecting DNA (DNA immunization). For this purpose, the target gene is first cloned into an expression vector so that the target sequence is under the control of a strong eukaryotic promoter (e.g. CMV promoter). Subsequently, DNA (e.g. 1-10 µg per injection) is transferred as immunogen using a gene gun into capillary regions with a strong blood flow in an organism (e.g. mouse, rabbit). The transferred DNA is taken up by the animal's cells, the target gene is expressed, and the animal finally develops an immune response to the target protein (Jung et al., *Mol. Cells* 12: 41-49, 2001; Kasinrerk et al., *Hybrid Hybridomics* 21: 287-293, 2002).

Production of Monoclonal Antibodies

Monoclonal antibodies are traditionally produced with the aid of the hybridoma technology (technical details: see "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142, "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447). A new method which is also used is the "SLAM" technology. Here, B cells are isolated from whole blood and the cells are made monoclonal. Subsequently the supernatant of the isolated B cell is analyzed for its antibody specificity. In contrast to the hybridoma technology, the variable region of the antibody gene is then amplified by single-cell PCR and cloned into a suitable vector. In this manner production of monoclonal antibodies is accelerated (de Wildt et al., J. Immunol. Methods 207:61-67, 1997).

5. Validation of the Targets by Protein-Chemical Methods Using Antibodies

The antibodies which can be produced as described above can be used to further analyze the target protein as follows:

Specificity of the Antibody

Assays based on cell culture with subsequent Western blotting are most suitable for demonstrating the fact that an antibody binds specifically only to the desired target protein (various variations are described, for example, in "Current Protocols in Protein Chemistry", John Wiley & Sons Ltd., Wiley InterScience). For the demonstration, cells are transfected with a cDNA for the target protein, which is under the control of a strong eukaryotic promoter (e.g. cytomegalovirus promoter; CMV). A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfecting cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). As an alternative, it is also possible to use cell lines which express the target gene endogenously (detection via target gene-specific RT-PCR). As a control, in the ideal case,

homologous genes are cotransfected in the experiment, in order to be able to demonstrate in the following Western blot the specificity of the analyzed antibody.

In the subsequent Western blotting, cells from cell culture or tissue samples which might contain the target protein are lysed in a 1% strength SDS solution, and the proteins are denatured in the process. The lysates are fractionated according to size by electrophoresis on 8-15% strength denaturing polyacrylamide gels (contain 1% SDS) (SDS polyacrylamide gel electrophoresis, SDS-PAGE). The proteins are then transferred by one of a plurality of blotting methods (e.g. semi-dry electroblot; Biorad) to a specific membrane (e.g. nitrocellulose, Schleicher & Schüll). The desired protein can be visualized on this membrane. For this purpose, the membrane is first incubated with the antibody which recognizes the target protein (dilution approx. 1:20-1:200, depending on the specificity of said antibody), for 60 minutes. After a washing step, the membrane is incubated with a second antibody which is coupled to a marker (e.g. enzymes such as peroxidase or alkaline phosphatase) and which recognizes the first antibody. It is then possible to make the target protein visible on the membrane in a color or chemi-luminescent reaction (e.g. ECL, Amersham Bioscience). An antibody with a high specificity for the target protein should in the ideal case only recognize the desired protein itself.

Localization of the Target Protein

Various methods are used to confirm the membrane localization, identified in the in silico approach, of the target protein. An important and well-established method using the antibodies described above is immunofluorescence (IF). For this purpose, cells of established cell lines which either synthesize the target protein (detection of the RNA by RT-PCR or of the protein by Western blotting) or else have been transfected with plasmid DNA are utilized. A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfection of cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). The plasmid transfected into the cells, in immunofluorescence, may encode the unmodified protein or else couple different amino acid markers to the target protein. The principle markers are, for example, the fluorescent green fluorescent protein (GFP) in various differentially fluorescent forms, short peptide sequences of 6-12 amino acids for which high-affinity and specific antibodies are available, or the short amino acid sequence Cys-Cys-X-X-Cys-Cys (SEQ ID NO: 636)which can bind via its cysteines specific fluorescent substances (Invitrogen). Cells which synthesize the target protein are fixed, for example, with paraformaldehyde or methanol. The cells may then, if required, be permeabilized by incubation with detergents (e.g. 0.2% Triton X-100). The cells are then incubated with a primary antibody which is directed against the target protein or against one of the coupled markers. After a washing step, the mixture is incubated with a second antibody coupled to a fluorescent marker (e.g. fluorescein, Texas Red, Dako), which binds to the first antibody. The cells labeled in this way are then overlaid with glycerol and analyzed with the aid of a fluorescence microscope according to the manufacturer's information. Specific fluorescence emissions are achieved in this case by specific excitation depending on the substances employed. The analysis usually permits reliable localization of the target protein, the antibody quality and the target protein being confirmed in double stainings with, in addition to the target protein, also the coupled amino acid markers or other marker proteins whose localization has already been described in the literature being stained. GFP and its derivatives represent a special case, being excitable

directly and themselves fluorescing. The membrane permeability which may be controlled through the use of detergents, in immunofluorescence, allows demonstration of whether an immunogenic epitope is located inside or outside the cell. The prediction of the selected proteins can thus be supported experimentally. An alternative possibility is to detect extracellular domains by means of flow cytometry. For this purpose, cells are fixed under non-permeabilizing conditions (e.g. with PBS/Na azide/2% FCS/5 mM EDTA) and analyzed in a flow cytometer in accordance with the manufacturer's instructions. Only extracellular epitopes can be recognized by the antibody to be analyzed in this method. A difference from immunofluorescence is that it is possible to distinguish between dead and living cells by using, for example, propidium iodide or trypan blue, and thus avoid false-positive results.

Another important detection is by immunohistochemistry (IHC) on specific tissue samples. The aim of this method is to identify the localization of a protein in a functionally intact tissue aggregate. IHC serves specifically for (1) being able to estimate the amount of target protein in tumor and normal tissues, (2) analyzing how many cells in tumor and healthy tissues synthesize the target gene, and (3) defining the cell type in a tissue (tumor, healthy cells) in which the target protein is detectable. Alternatively, the amounts of protein of a target gene may be quantified by tissue immunofluorescence using a digital camera and suitable software (e.g. Tillvision, Till-photonics, Germany). The technology has frequently been published, and details of staining and microscopy can therefore be found, for example, in "Diagnostic Immunohistochemistry" by David J., MD Dabbs ISBN: 0443065667 or in "Microscopy, Immunohistochemistry, and Antigen Retrieval Methods: For Light and Electron Microscopy" ISBN: 0306467704. It should be noted that, owing to the properties of antibodies, different protocols have to be used (an example is described below) in order to obtain a meaningful result.

Normally, histologically defined tumor tissues and, as reference, comparable healthy tissues are employed in IHC. It is also possible to use as positive and negative controls cell lines in which the presence of the target gene is known through RT-PCR analyses. A background control must always be included.

Formalin-fixed (another fixation method, for example with methanol, is also possible) and paraffin-embedded tissue pieces with a thickness of 4 μm are applied to a glass support and deparaffinated with xylene, for example. The samples are washed with TBS-T and blocked in serum. This is followed by incubation with the first antibody (dilution: 1:2 to 1:2000) for 1-18 hours, with affinity-purified antibodies normally being used. A washing step is followed by incubation with a second antibody which is coupled to an alkaline phosphatase (alternative: for example peroxidase) and directed against the first antibody, for approx. 30-60 minutes. This is followed by a color reaction using alkaline phosphatase (cf., for example, Shi et al., *J. Histochem. Cytochem.* 39: 741-748, 1991; Shin et al., *Lab. Invest.* 64: 693-702, 1991). To demonstrate antibody specificity, the reaction can be blocked by previous addition of the immunogen.

Analysis of Protein Modifications

Secondary protein modifications such as, for example, N- or O-glycosylations or myristilations may impair or even completely prevent the accessibility of immunogenic epitopes and thus call into question the efficacy of antibody therapies. Moreover, it has frequently been demonstrated that the type and amount of secondary modifications differ in normal and tumor tissues (e.g. Durand & Seta, 2000; Clin.

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Chem. 46: 795-805; Hakomori, 1996; Cancer Res. 56: 5309-18). The analysis of these modifications is therefore essential to the therapeutic success of an antibody. Potential binding sites can be predicted by specific algorithms.

Analysis of protein modifications usually takes place by Western blotting (see above). Glycosylations which usually have a size of several kDa, especially lead to a larger total mass of the target protein, which can be fractionated in SDS-PAGE. To detect specific O- and N-glycosidic bonds, protein lysates are incubated prior to denaturation by SDS with O- or N-glycosylases (in accordance with their respective manufacturer's instructions, e.g. PNgase, endoglycosidase F, endoglycosidase H, Roche Diagnostics). This is followed by Western blotting as described above. Thus, if there is a reduction in the size of a target protein after incubation with a glycosidase, it is possible to detect a specific glycosylation and, in this way, also analyze the tumor specificity of a modification.

Functional Analysis of the Target Gene

The function of the target molecule may be crucial for its therapeutic usefulness, so that functional analyses are an important component in the characterization of therapeutically utilizable molecules. The functional analysis may take place either in cells in cell culture experiments or else in vivo with the aid of animal models. This involves either switching off the gene of the target molecule by mutation (knockout) or inserting the target sequence into the cell or the organism (knockin). Thus it is possible to analyze functional modifications in a cellular context firstly by way of the loss of function of the gene to be analyzed (loss of function). In the second case, modifications caused by addition of the analyzed gene can be analyzed (gain of function).

a. Functional Analysis in Cells

Transfection. In order to analyze the gain of function, the gene of the target molecule must be transferred into the cell. For this purpose, cells which allow synthesis of the target molecule are transfected with a DNA. Normally, the gene of the target molecule here is under the control of a strong eukaryotic promoter (e.g. cytomegalovirus promoter; CMV). A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfecting cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). The gene may be synthesized either transiently, without genomic integration, or else stably, with genomic integration after selection with neomycin, for example.

RNA interference (siRNA). An inhibition of expression of the target gene, which may induce a complete loss of function of the target molecule in cells, may be generated by the RNA interference (siRNA) technology in cells (Hannon, G J. 2002. RNA interference. Nature 418: 244-51; Czauderna et al. 2003. Nucl. Acid Res. 31: 670-82). For this purpose, cells are transfected with short, double-stranded RNA molecules of approx. 20-25 nucleotides in length, which are specific for the target molecule. An enzymic process then results in degradation of the specific RNA of the target gene and thus in reduced expression of the target protein and consequently enables the target gene to be functionally analyzed.

Cell lines which have been modified by means of transfection or siRNA may subsequently be analyzed in different ways. The most common examples are listed below.

1. Proliferation and Cell Cycle Behavior

A multiplicity of methods for analyzing cell proliferation are established and are commercially supplied by various companies (e.g. Roche Diagnostics, Invitrogen; details of the assay methods are described in the numerous application protocols). The number of cells in cell culture experiments

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can be determined by simple counting or by colorimetric assays which measure the metabolic activity of the cells (e.g. wst-1, Roche Diagnostics). Metabolic assay methods measure the number of cells in an experiment indirectly via enzymic markers. Cell proliferation may be measured directly by analyzing the rate of DNA synthesis, for example by adding bromodeoxyuridine (BrdU), with the integrated BrdU being detected colorimetrically via specific antibodies.

2. Apoptosis and Cytotoxicity

A large number of assay systems for detecting cellular apoptosis and cytotoxicity are available. A decisive characteristic is the specific, enzyme-dependent fragmentation of genomic DNA, which is irreversible and in any case results in death of the cell. Methods for detecting these specific DNA fragments are commercially obtainable. An additional method available is the TUNEL assay which can detect DNA single-strand breaks also in tissue sections. Cytotoxicity is mainly detected via an altered cell permeability which serves as marker of the vitality state of cells. This involves on the one hand the analysis of markers which can typically be found intracellularly in the cell culture supernatant. On the other hand, it is also possible to analyze the absorbability of dye markers which are not absorbed by intact cells. The best-known examples of dye markers are Trypan blue and propidium iodide, a common intracellular marker is lactate dehydrogenase which can be detected enzymatically in the supernatant. Different assay systems of various commercial suppliers (e.g. Roche Diagnostics, Invitrogen) are available.

3. Migration Assay

The ability of cells to migrate is analyzed in a specific migration assay, preferably with the aid of a Boyden chamber (Corning Costar) (Cinamon G., Alon R. J. Immunol. Methods. 2003 February; 273(1-2):53-62; Stockton et al. 2001. Mol. Biol. Cell. 12: 1937-56). For this purpose, cells are cultured on a filter with a specific pore size. Cells which can migrate are capable of migrating through this filter into another culture vessel below. Subsequent microscopic analysis then permits determination of a possibly altered migration behavior induced by the gain of function or loss of function of the target molecule.

b. Functional Analysis in Animal Models

A possible alternative of cell culture experiments for the analysis of target gene function are complicated in vivo experiments in animal models. Compared to the cell-based methods, these models have the advantage of being able to detect faulty developments or diseases which are detectable only in the context of the whole organism. A multiplicity of models for human disorders are available by now (Abate-Shen & Shen. 2002. Trends in Genetics S1-5; Matsusue et al. 2003. J. Clin. Invest. 111:737-47). Various animal models such as, for example, yeast, nematodes or zebra fish have since been characterized intensively. However, models which are preferred over other species are mammalian animal models such as, for example, mice (*Mus musculus*) because they offer the best possibility of reproducing the biological processes in a human context. For mice, on the one hand transgenic methods which integrate new genes into the mouse genome have been established in recent years (gain of function; Jegstrup I. et al. 2003. Lab Anim. 2003 Jan.; 37(1):1-9). On the other hand, other methodical approaches switch off genes in the mouse genome and thus induce a loss of function of a desired gene (knockout models, loss of function; Zambrowicz B P & Sands A T. 2003. Nat. Rev. Drug Discov. 2003 January; 2(1):38-51; Niwa H. 2001. Cell Struct. Funct. 2001 June; 26(3):137-48); technical details have been published in large numbers.

After the mouse models have been generated, alterations induced by the transgene or by the loss of function of a gene can be analyzed in the context of the whole organism (Balling R, 2001. Ann. Rev. Genomics Hum. Genet. 2:463-92). Thus it is possible to carry out, for example, behavior tests as well as to biochemically study established blood parameters. Histological analyses, immunohistochemistry or electron microscopy enable alterations to be characterized at the cellular level. The specific expression pattern of a gene can be detected by in-situ hybridization (Peters T. et al. 2003. Hum. Mol. Genet 12:2109-20).

Example 3

Detailed Analysis of the Identified Tumor-Associated Markers

RNA-Isolation, RT-PCR and Real-Time RT-PCR

RNA extraction, first-strand cDNA synthesis, RT-PCR and real-time RT-PCR was performed as previously described (Koslowski, M. et al., Cancer Res. 62, 6750-6755 (2002), Koslowski, M. et al., Cancer Res. 64, 5988-5993 (2004)). Real-time quantitative expression analysis was performed in a 40 cycle RT-PCR. After normalization to HPRT (sense 5'-TGA CAC TGG CAA AAC AAT GCA-3'(SEQ ID NO: 628)); antisense 5'-GGT CCT TTT CAC CAG CAA GCT-3' (SEQ ID NO: 629), 62° C. annealing) gene-specific transcripts in tumor samples were quantified relative to normal tissues using ΔΔCT calculation.

siRNA Duplexes

The SEQ ID NO:540 siRNA duplexes (Qiagen, Hilden, Germany) were directed against target sequences 5'-NNC CAC AGA AGG UAC CAG UUA-3' (SEQ ID NO: 634) (siRNA#1; sense (5'-CCA CAG AAG GUA CCA GUU AUU-3' (SEQ ID NO: 630)), antisense (5'-UAA CUG GUA CCU UCU GUG GUU-3' (SEQ ID NO: 631)) and 5'-NNC AGC AAG ACU CCC UCU AAA-3' (SEQ ID NO: 635) (siRNA#2; sense (5'-CAG CAA GAC UCC CUC UAA AUU-3' (SEQ ID NO: 632)), antisense (5'-UUU AGA GGG AGU CUU GCU GUU-3' (SEQ ID NO: 633)) of the SEQ ID NO:540 mRNA sequence.

Cell Proliferation Analysis

24 h after transfection with siRNA duplexes 1×10^4 cells were cultured for 48 h in medium supplemented with 10% FCS. Proliferation was analyzed by measuring the incorporation of BrdU into newly synthesized DNA strands using the DELFIA cell proliferation Kit (Perkin Elmer, Boston, Mass.) according to the manufacturer's instructions on a Wallac Victor^2 multi-label counter (Perkin Elmer, Boston, Mass.).

FIG. 3 shows the quantification of SEQ ID NO:540 mRNA expression in MCF-7 breast cancer cells by real-time RT-PCR 24 h after transfection with siRNA oligos. Compared to non-transfected cells and cells transfected with non-silencing (ns) siRNA both SEQ ID NO:540-specific siRNAs (siRNA#1 (SEQ ID NO:630, 631), siRNA#2 (SEQ ID NO:632, 633)) induce robust silencing of SEQ ID NO:540 expression.

FIG. 4 shows that silencing of SEQ ID NO:540 expression by transfection with siRNA oligos results in impaired proliferation of MCF-7 breast cancer cells. Proliferation was quantified 96 h after transfection with siRNAs by measuring incorporation of BrdU in newly synthesized DNA strands. These results show that SEQ ID NO:540 is a positive factor for the proliferation of breast cancer cells.

The nucleotide sequence according to SEQ ID NO:541 was deduced from SEQ ID NO:65 and codes for a 177 aa protein (SEQ ID NO:542) of unknown function. Expression of SEQ ID NO:541 in normal and cancerous tissues was

quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:543, 544); see FIG. 5. In normal tissues SEQ ID NO:541 is highly expressed in placenta and shows only weak expression in thymus. SEQ ID NO:541 is overexpressed in lung cancer. Based on these expression results, SEQ ID NO:541 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

The nucleotide sequence according to SEQ ID NO:545 was deduced from SEQ ID NO:249 and codes for a member of the solute carrier (SLC) group of membrane proteins (SEQ ID NO:546). As is typical of integral membrane proteins, SLCs contain a number of hydrophobic transmembrane alpha helices connected to each other by hydrophilic intra- or extra-cellular loops. Depending on the SLC, these transporters are functional as either monomers or obligate homo- or hetero-oligomers. The protein encoded by SEQ ID NO:545 is a cell surface protein. Expression of SEQ ID NO:545 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:547, 548); see FIG. 6. Compared to normal tissues, SEQ ID NO:545 is overexpressed in malignant melanomas. Based on these expression results, SEQ ID NO:545 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

The nucleotide sequence according to SEQ ID NO:549 was deduced from SEQ ID NO:4 and codes for a 763 aa protein (SEQ ID NO:550) of unknown function. The protein harbors two potential transmembrane domains and a typical fibronectin type III domain. Fibronectin is a high-molecular-weight extracellular matrix glycoprotein that binds to membrane spanning receptor proteins (integrins). In addition to integrins, they also bind extracellular matrix components such as collagen, fibrin and heparan sulfate. The protein encoded by SEQ ID NO:549 might represent a hitherto unknown new fibronection-like protein. Expression of SEQ ID NO:549 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:551, 552); see FIG. 7. Compared to normal tissues, SEQ ID NO:549 is overexpressed in ovarian cancer. Based on these expression results, SEQ ID NO:549 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular of this particular tumor type.

The nucleotide sequence according to SEQ ID NO:553 was deduced from SEQ ID NO:156 and codes for a 496 aa protein (SEQ ID NO:554) of unknown function. The protein harbors a potential transmembrane protein. Expression of SEQ ID NO:553 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:555, 556); see FIG. 8. In normal tissues SEQ ID NO:553 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:553 is overexpressed in colon cancer and ovarian cancer. Based on these expression results, SEQ ID NO:553 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:557 was deduced from SEQ ID NO:273. SEQ ID NO:557 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:557 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:558, 559); see FIG. 9. In normal tissues high expression of SEQ ID NO:557 is detectable in breast. Compared to normal tissues, SEQ ID NO:557 is overexpressed in breast cancer. Based on these expression results, SEQ ID NO:557 and its expression products qualify as

molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

The nucleotide sequence according to SEQ ID NO:560 was deduced from SEQ ID NO:135. SEQ ID NO:560 has no apparent open reading frame. Expression of SEQ ID NO:560 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:561, 562); see FIG. **10**. In normal tissues expression of SEQ ID NO:560 is detectable in duodenum and colon. Compared to normal tissues, SEQ ID NO:560 is overexpressed in colon cancer and ovarian cancer. Based on these expression results, SEQ ID NO:560 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:563 was deduced from SEQ ID NO:177. SEQ ID NO:563 has no apparent open reading frame. Expression of SEQ ID NO:563 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:564, 565); see FIG. **11**. SEQ ID NO:563 is highly expressed in placenta. Compared to normal tissues, SEQ ID NO:563 is overexpressed in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:563 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:566 was deduced from SEQ ID NO:149 and codes for a 155 aa protein (SEQ ID NO:567) of unknown function. The protein sequence is partially homologous to members of the tumor necrosis factor receptor superfamily and harbors a potential transmembrane domain. The protein encoded by SEQ ID NO:566 might represent a new member of the tumor necrosis factor receptor superfamily. Expression of SEQ ID NO:566 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:568, 569); see FIG. **12**. Compared to normal tissues, SEQ ID NO:566 is overexpressed in gastric cancer, breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:566 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:570 was deduced from SEQ ID NO:53 and codes for a member of the kernel lipocain superfamily (SEQ ID NO:571). These secreted glycoproteins have distinct and essential roles in regulating an uterine environment suitable for pregnancy and in the timing and occurrence of the appropriate sequence of events in the fertilization process. Expression of SEQ ID NO:570 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:572, 573); see FIG. **13**. SEQ ID NO:570 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:570 is overexpressed in ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:570 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:574 has no apparent open reading frame. Expression of SEQ ID NO:574 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:575, 576); see FIG. **14**. SEQ ID NO:574 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:574 is overexpressed in lung cancer and melanoma. Based on these expression results, SEQ ID NO:574

and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:577 was deduced from SEQ ID NO:20. SEQ ID NO:577 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:577 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:578, 579); see FIG. **15**. SEQ ID NO:577 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:577 is overexpressed in gastric cancer, breast cancer and lung cancer. Based on these expression results, SEQ ID NO:577 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:580 was deduced from SEQ ID NO:32. SEQ ID NO:580 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:580 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:581, 582); see FIG. **16**. SEQ ID NO:580 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:580 is overexpressed in ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:580 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:583 was deduced from SEQ ID NO:257 and codes for a member of the homeobox class of transcription factors (SEQ ID NO:584). Expression of these proteins is spatially and temporally regulated during embryonic development. Expression of SEQ ID NO:583 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:585, 586); see FIG. **17**. SEQ ID NO:583 is highly expressed in placenta and prostate. Compared to other normal tissues, SEQ ID NO:583 is overexpressed in colon cancer, ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:583 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:587 was deduced from SEQ ID NO:148 and codes for a member of the IGF-II mRNA-binding protein (IMP) family (SEQ ID NO:588). It functions by binding to the 5' UTR of the insulin-like growth factor 2 (IGF2) mRNA and regulating IGF2 translation. Expression of SEQ ID NO:587 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:589, 590); see FIG. **18**. Compared to normal tissues, SEQ ID NO:587 is overexpressed in lung cancer. Based on these expression results, SEQ ID NO:587 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

The nucleotide sequence according to SEQ ID NO:591 was deduced from SEQ ID NO:194 and codes for a 372 aa protein (SEQ ID NO:592) of unknown function. Expression of SEQ ID NO:591 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:593, 594); see FIG. **19**. SEQ ID NO:591 is highly expressed in testis. Compared to other normal tissues, SEQ ID NO:591 is overexpressed in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:591 and its expression

products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:595 was deduced from SEQ ID NO:191 and codes for a 357 aa protein (SEQ ID NO:596) of unknown function. Expression of SEQ ID NO:595 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:597, 598); see FIG. **20**. SEQ ID NO:595 is highly expressed in testis. Compared to other normal tissues, SEQ ID NO:595 is overexpressed in gastric cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:595 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:599 was deduced from SEQ ID NO:18 and has no apparent open reading frame. Expression of SEQ ID NO:599 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:600, 601); see FIG. **21**. SEQ ID NO:599 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:599 is overexpressed in gastric cancer, breast cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:599 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:602 was deduced from SEQ ID NO:133 and codes for a member of the von Willebrand factor domain superfamily of extracellular matrix proteins (SEQ ID NO:603). Expression of SEQ ID NO:602 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:604, 605); see FIG. **22**. Compared to normal tissues, SEQ ID NO:602 is overexpressed in ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:602 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:606 was deduced from SEQ ID NO:128 and codes for a member of the Borg family of CDC42 effector proteins (SEQ ID NO:607). Borg family proteins contain a CRIB (Cdc42/Rac interactive-binding) domain. They bind to, and negatively regulate the function of CDC42. CDC42, a small Rho GTPase, regulates the formation of F-actin-containing structures through its interaction with the downstream effector proteins. Expression of SEQ ID NO:606 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:608, 609); see FIG. **23**. Compared to normal tissues, SEQ ID NO:606 is overexpressed in gastric cancer, colon cancer and lung cancer. Based on these expression results, SEQ ID NO:606 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:610 was deduced from SEQ ID NO:118 and has no apparent open reading frame. Expression of SEQ ID NO:610 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:611, 612); see FIG. **24**. Compared to normal tissues, SEQ ID NO:610 is overexpressed in gastric cancer, breast cancer and lung cancer. Based on these expression results, SEQ ID NO:610 and its

expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:613 was deduced from SEQ ID NO:116 and codes for a 76 aa protein (SEQ ID NO:614) of unknown function. Expression of SEQ ID NO:613 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:615, 616); see FIG. **25**. SEQ ID NO:613 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:613 is overexpressed in breast cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:613 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:617 was deduced from SEQ ID NO:267. SEQ ID NO:617 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:617 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:618, 619); see FIG. **26**. SEQ ID NO:617 is highly expressed in placenta and endometrium. Compared to other normal tissues, SEQ ID NO:617 is overexpressed in lung cancer and melanoma. Based on these expression results, SEQ ID NO:617 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:620 was deduced from SEQ ID NO:182 and codes for a 829 aa protein (SEQ ID NO:621) harboring multiple putative transmembrane domains and a patched family domain. The transmembrane protein Patched is a receptor for the morphogene Sonic Hedgehog. This protein associates with the smoothened protein to transduce hedgehog signals. SEQ ID NO:620 might represent a novel member of the Patched family. Expression of SEQ ID NO:620 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:622, 623); see FIG. **27**. SEQ ID NO:620 is highly expressed in lung. Compared to other normal tissues, SEQ ID NO:620 is overexpressed in ovarian cancer and melanoma. Based on these expression results, SEQ ID NO:620 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The nucleotide sequence according to SEQ ID NO:624 was deduced from SEQ ID NO:184 and codes for a 323 aa protein (SEQ ID NO:625) similar to TWIK-related acid-sensitive K^+ channel, a member of the superfamily of potassium channel proteins that contain two pore-forming P domains. Expression of SEQ ID NO:624 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:626, 627); see FIG. **28**. SEQ ID NO:624 is highly expressed in lung. Compared to other normal tissues, SEQ ID NO:624 is overexpressed in gastric cancer and lung cancer. Based on these expression results, SEQ ID NO:624 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

The presently described technology is now described in such full, clear, concise and exact terms as to enable any person skilled in the art to which it pertains, to practice the same. It is to be understood that the foregoing describes preferred embodiments of the technology and that modifications may be made therein without departing from the spirit or scope of the invention as set forth in the appended claims.

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

ttacccttca ttcacctatt acggttcagg agaaaacctc gacttgtcct gcttcacgga      60

atctaaccca ccggcagagt attttttggac aattaatggg aagtttcagc aatcaggaca     120

aaagctcttt atcccccaaa ttactagaaa tcatagcggg ctctatgttt gctctgttca     180

taactcagcc actggcaagg aaatctccaa atccatgaca gtcaaagtct ctggtccctg     240

ccatggagac ctgacagagt ttcagtcatg actgcaacaa ctgagacact gagaaaaaga     300

acaggctgat accttcatga aattcaagac aaagaagaaa aaaactcaat gttattggac     360

taaataatca aaaggataat gttttcataa ttttttattg gaaaatgtgc tgattctttg     420

aatgttttat tctccagatt tatgaacttt ttttcttcag caattggtaa agtatacttt     480

tgtaaacaaa aattgaaata tttgcttttg ctgtctatct gaatgcccca gaattgtgaa     540

actactc                                                             547


<210> SEQ ID NO 10
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

gcaggggacg caccaaggat ggagatgttc caggggctgc tgctgttgct gctgctgagc      60

atgggcggga catgggcatc caaggagccg cttcggccac ggtgccgccc catcaatgcc     120

accctggctg tggagaagga gggctgcccc gtgtgcatca ccgtcaacac caccatctgt     180

gccggctact gccccaccat gacccgcgtg ctgcaggggg tcctgccggc cctgcctcag     240

gtggtgtgca actaccgcga tgtgcgcttc gagtccatcc ggctccctgg ctgcccgcgc     300
```

```
ggcgtgaacc ccgtggtctc ctacgccgtg gctctcagct gtcaatgtgc actctgccgc     360

cgcagcacca ctgactgcgg gggtcccaag gaccac                                396
```

```
<210> SEQ ID NO 11
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

aaatggtggt gtttgactgg tatatgacct tcctctggag gtgatcaacc agtaagggaa      60

aatcgctcca agtgagcatg cacacaacct cagtaaacac actgtgcatg tggcttctcc     120

caagtactag caggccactg cacatgtcac aactgagcaa cagcccaccc caatggaggg     180

atcaagggag gagaagaaaa accccggaac caaaagccag tttataaaaa tcctgagcca     240

aaggctgagg ggggcacttg atctctcaag ttccctactt ggccctcttc caagtgtgat     300

ttgcttcttt t                                                          311
```

```
<210> SEQ ID NO 12
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (184)..(184)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 12

gccttagccc ccgggattta gagcatcctc gcgaccaccc ggaggcttct gggggccact      60

ctgcggatga ggaagctgac gcctgggtgc agaaccccgg accccgagat tcagagccca     120

ggtccagccg cgcttccgca caaacttgcg ctcggagcaa gtcccctcct tcccagcact     180

catntgagac cagaggtgtc cccaccgtcc ccgctagcag cgctggttat attgtgggcc     240

aacctt                                                                246
```

```
<210> SEQ ID NO 13
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (149)..(150)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (153)..(159)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (161)..(163)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (168)..(184)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 13

cctttttgctt gagcagggtt cccaggaggg agaaagagaa gacaagagcc tgatgcccaa      60

ctttgtgtgt gtggggacgg gggagtcagg gcccccaag tcccacaata gccccaatgt     120
```

```
ttgcctatcc acctccccca agcccctttnn ccnnnnnnnc nnntnacnnn nnnnnnnnnn      180

nnnnctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg gactggtcgg      240

tgcccagaaa gtctcttctg ccactgacgc ccccatcagg gattgggcct tctttccccc      300

ttcctttctg tgtctcctgc ctcatcggcc tgccatgacc tgcagccaag cccagccccg      360

tggggaaggg gagaaagtgg gggatggcta agaaagctgg gagatatggga acagaagagg     420

gtagtgggtg ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta      480

atttatacaa agatattaag gccctgttca ttaaga                               516
```

```
<210> SEQ ID NO 14
<211> LENGTH: 162
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 14

gagcctagag agtaaggaac gttatatagt tttccccaaa ggttcacttg aaagaacttt       60

tcattggttg tcatggtagt aatgtcctga tnttgaaatc tcccagaacc tagtagctct      120

taaacatgct ttcatcttgg ttcctttggt ctgacggaaa ct                        162
```

```
<210> SEQ ID NO 15
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 15

tttgcaaaag gtttccggga cactggaaat ggccgaagag aaaaaagana acagctcacc       60

ctgcagtcca tgagggtgtt tgatgaaaga cacaaaaagg agaatgggac ctctgatgag      120

tcctccagtg aacaagcagc tttcaactgc ttcgcccagg cttcttctcc agccgcctcc      180

actgtaggga catcgaacct caaagattta tgtcccagcg agggtgagag cgacgccgag      240

gccgagagca aagaggagca tggccccgag gcctgcgacg cggccaagat ctccaccacc      300

acgtcggagg agccctgccg tgacaagggc agccccgcgg tcaaggctca ccttttcgct      360

gctgagcggc cccgggacag cgggcggctg gacaaagcgt cgcccgactc acgccatagc      420

cccgccacca tctcgtccag cactcgcggc ctgggcgcgg aggagcgcag gagcccggtt      480

cgcgagggca cagcgccggc caaggtggaa gaggcgcgcg cgc                       523
```

```
<210> SEQ ID NO 16
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

actcggtcac actcagtaag tccttgcaga gtccatgggt ttcttcgaca agtggcttca       60

aggaagggaa ttcccacccct tgtcttccag caaggccaca cacatgaaac cagcagaaaa     120

gagtcttatt tgctggaaag accccccagca agggcatagt gagcccttac agtggttcca     180

gtcagaaaag gcaccacttg ggtgggcaca gccccatggt tgtccaactt ggtaagcaga      240

gcaaggctgg acttgagtcc ccgtcctcca caaaacacag agccacaagc cccagccctg      300
```

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```
cagcagccct ccggaagcag cggggcactg gtttccttgt cccctgccat ctaccgagtg     360

gctcactctc aggtgggagt gctggtgatg gttaattagg actgcagaaa catgagcctc     420

ctta                                                                 424


<210> SEQ ID NO 17
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

ctatctttct ggtcacattg tcggtgtttc tgcatgttct ccattccgct cctgatgtgc      60

aggattgccc agaatgcacg ctacaggaaa acccattctt ctcccagccg ggtgccccaa     120

tacttcagtg catgggctgc tgcttctcta gagcatatcc cactccacta aggtccaaga     180

agacgatgtt ggtccaaaag aacgtcacct cagagtccac ttgctgtgta gctaaatcat     240

ataacagggt cacagtaatg gggggtttca aagtggagaa ccacacggcg tgccactgca     300

gtacttgtta ttatcacaaa tcttaaatgt tttaccaagt gctgtcttga tgactgctga     360

ttttctggaa tggaaaatta agttgtttag tgtttatggc tttgtgagat aaaactctcc     420

ttttccttac cataccactt tgacacgctt caaggatata ctgcagcttt actgccttcc     480

tccttatcct acagtacaat cagcagtcta gttcttttca tttg                     524


<210> SEQ ID NO 18
<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

gtagggcgaa ctctgctata cagtttatga tgtcagagtg aatactttct ttgagttgca      60

gtcagaaact gtagattttt aaaaatttaa aattcattat tctctgtcag tattccaaag     120

tgtatacaga aagctattgc actgttcagg agatggcgct taacattttg gaaattcaag     180

gtgatgaatg tccagataag actatctctc ctggtacaaa gtttgacaat gctgaacatt     240

tttaaaggtt cttttttgata tacaaagtgc accaatgagt gcttttttaat tcttacaata     300

attctgggtg aggtaggtat ttttccaatt cccattttat gcttcggtag ccctttgtat     360

ttatacttca aaacacttgg ctctcttgta attatttaag aaattagttg tgattatttg     420

tttaatgtgc aggagttaca aaaggcaagc tttagaacaa gacagacctg gttatgattc     480

ctggctctga aagctgtaca ccctgtgacc ctagacaggt gttttaatgc ctcgctgc       538


<210> SEQ ID NO 19
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (294)..(295)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 19

tcttggtctt ctgctcatgg atgacgcacc agtcgtgcat gttcttggtg aagtcggcca      60

gcctgagcaa gcggaggacc tacgccggcc tggcattcca cgcctacggg aaggcaggca     120

agatgctggt ggagaccagc atgatcgggc tgatgctggg cacctgcatc gccttctacg     180

tcgtgatcgg cgacttgggg tccaacttct ttgcccggct gttcgggttt caggtgggcg     240
```

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gcaccttccg catgttcctg ctgttcgccg tgtcgctgtg catcgtgctc ccgnncagcc      300

tgcagcggaa catgatggcc tcca                                            324


<210> SEQ ID NO 20
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

agaaagcaga gcagcctcct ggaagaaggc cttgtcagct ttgtctgtgc ctcgcaaatc       60

agaggcaagg gagaggttgt taccagggga cactgagaat gtacatttga tctgccccag      120

ccacggaagt cagagtagga tgcacagtac aaaggagggg ggagtggagg cctgagaggg      180

aagtttctgg agttcagata ctctctgttg ggaacaggac atctcaacag tctcaggttc      240

gatcagtggg tcttttggca ctttgaacct tgaccacagg gaccaagaag tggcaatgag      300

gacacctgca ggagggcta gcctgactcc cagaacttta agactttctc cccactgcct      360

tctgctgcag cccaagcagg gagtgtcccc ctcccagaag catatcccag atga            414


<210> SEQ ID NO 21
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

caaagtcatc tgaacttccg tttccccagg gcctccagct gccctcagac actgatgtct       60

gtccccaggt gctctctgcc cctcatgccc ctctcaccgg cccagtgccc cgactctcca      120

ggctttatca aggtgctaag gcccgggtgg gcagctcctc gtctcagagc cctcctccgg      180

cctggtgctg cctttacaaa cacctgcagg agaaggggcca cggaagcccc aggctttaga      240

gccctcagca ggtctgggga gctagagcaa aggagggacc tcaggccttc cgtttcttct      300

tccagggtgg ggtggcctgg tgttcccta gccttccaaa cccaggtggc ctgcccttct      360

ccccagaggg aggcggcctc cgcccattgg tgctcatgca gactctgggg ctgaggtgcc      420

ccggggggtg atctctggtg ctcacagccg agggagccgt ggctccatgg ccagatgacg      480

gaaacagggt ctgaccaagt gccaggaaga cctgtgctat aaaccaccct g               531


<210> SEQ ID NO 22
<211> LENGTH: 522
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

atgtcctgcc atttggtcat aagacagttg catttactct gctaccattg cttcagttga       60

tatgaagaga gaaagctgtg ttgtgattta cactggatat ggaaatagag aggaacaaat      120

ctgtctgatc tactttcttc aacctctgta gtagctaata atataggaca gaatgctcca      180

aagaatgaaa atgaaagtca agattcaatg gatgaaagtg agaactcctc caggtcctgg      240

aaacaaacca tttagcatca ggtcagaagc tactccatgg aattctgaga ccacgaaagc      300

caggtcaggt ctcaaattca gtagcccacc acccacacca ccaccacac caccctgctt      360

cccctcatgc ttgctgcctc catttccttc tggaccacca ataattcccc caccacctcc      420

cacaggtcta gattttcttg atgatgttaa tgttttatga agtatgctaa tctcttggta      480

cattaagtgg ctatcatact ggctattata cagggctcaa gc                        522
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<210> SEQ ID NO 23
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (98)..(98)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (142)..(142)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 23

gaaaggcctg caattgtgtc ttcacgatgc ttttccaaga cagccaaggc aggtataatt        60

ttcctcagca agaaagagga acctcggagg tgtgcacngc ctggctggcc acccaggtat       120

tggcaaaagt gactgtcggg cntgctggcc cggcccccgc ccgccgtccc tggagcactc       180

acgatgcggt ccggcggcgg cgtgctccgg atgaagcact tgatctggcc cttctcgccg       240

tggagggcgt gctgggtctg ggtgctggag atgatggggg gtcctgttga gaaacagcgt       300

cccattaggc acccgggaag ggcacgtccc tgctggcgcc ctcttgggtg ggttcagaag       360

tgtattcatt aatccaagca ttcagcaaac atttgccgaa ggcctgtatg tgcaaggtaa       420

agtgcaaggt agaggactca gagataaatt aggcattcag tcataaacct ctcaagggat       480

catgagcgaa tgcttctaag tcagaacccc cagaagatac                             520


<210> SEQ ID NO 24
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

agcagaacct cctagggttt ctccttccac tccttgccat gatcttcttc tactcccgta        60

ttggttgtgt cttggtgagg ctgaggcccg caggccaggg ccgggcttta aaaatagctg       120

cagccttggt ggtggccttc ttcgtgctat ggttcccata caatctcacc ttgtttctgc       180

atacgctgtt ggacctgcaa gtattcggga actgtgaggt cagccagcat ctagactacg       240

cactccaggt aacagagagc atcgccttcc ttcactgctg cttttccccc atcctgtatg       300

ccttctccag tcaccgcttc cgccagtacc tgaaggcttt cctggctgcc gtgcttggat       360

ggcacctggc acctggcact gcccaggcct cattatccag ctgttctgag agcagcatac       420

ttactgccct tgaggaaatg actggcatga atgaccttgg agagaggcag tctgagaact       480

accctaac                                                               488


<210> SEQ ID NO 25
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

gaggagagac ctgcgtggga taatcaacag gggtctggag gacggggaga gctgggaata        60

tcagatctga ctgcgtgttc tcacttcgct tcctggaact tgctctcatt ttcctgggtg       120

catcaaacaa aacaaaaacc aaacacccag aggtctcatc tcccaggccc caggggagaa       180

agaggagtag catgaacgcc aaggaatgta cgttgagaat cactgctcca ggcctgcatt       240

actccttcag ctctgggca gaggaagccc agcccaagca cggggctggc agggcgtgag        300

gaactctcct gtggcctgct catcaccctt ccgacaggag cactgcatgt cagagcactt       360
```

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```
taaaaacagg ccagcctgct tgggcgctcg gtctccaccc cagggtcata agtggggaga      420

gagcccttcc cagggcaccc aggcaggtgc agggaagtgc agagcttgtg gaaagcgtgt      480

gagtgaggga gacaggaacg gctctggggg tgggaagtgg ggctaggtct tgccaactcc      540

atcttcaata aa                                                          552
```

```
<210> SEQ ID NO 26
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

aagcctcaag gcacttctag gacctggctc ttctcaccaa gatgaactca ctggtttctt       60

ggcagctact gcttttcctc tgtgccaccc actttgggga gccattagaa aaggtggcct      120

ctgtggggaa ttctagaccc acaggccagc agctagaatc cctgggcctc ctggcccccg      180

gggagcagag cctgccgtgc accgagagga agccagctgc tactgccagg ctgagccgtc      240

gggggacctc gctgtccccg cccccgaga gctccgggag ccgccagcag ccgggcctgt        300

ccgcccccca cagccgccag atccccgcac cccagggcgc ggtgctggtg cagcgggaga      360

aggacctgcc gaactacaac tggaactcct tcggcctgcg cttcggcaag cgggaggcgg      420

caccagggaa ccacggcaga agcgctgggc ggggctgggg cgcaggtgcg gggcagtgaa      480

cttcagaccc caaaggagtc agagcatgcg g                                     511
```

```
<210> SEQ ID NO 27
<211> LENGTH: 131
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

ctcctccagc aagacagatg cctagcccgt cctcaggaat ctgccgccag ggagaatggc       60

aaccctggcc agatagctgg aagcacaggg ttgctcttca acctgcctcc cggctcagtt      120

cactataaga a                                                           131
```

```
<210> SEQ ID NO 28
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 28

tttcctctga gagaacagcg gtcttctgtc tgctgtggca nagcaagtca cttcttcttg        60

tagtgagaac tgaaaccaga accnatcatg tgccacttcc tggacacctc ctattaaata      120

ttaaagtcct ctcaccacag aagccggagt ttagtggtta ggggcacagg ttcttagata      180

tgaacatcag ttgcaaccta ccaactgcat gctcttggac aatttacatt tctgtgtatc      240

agctttcctt tttctttaga atgagatatt aatagtagca acccagaatt gtcatgaagc      300

ctaa                                                                   304
```

```
<210> SEQ ID NO 29
<211> LENGTH: 226
```

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

catggcaaag gcttgcccca aatctcaact tctcagacgt tccataccc cacatgccaa      60

tttcagcacc caactgagat ccgaggagct cctgggaagc cctgggtgca ggacactggt     120

cgagagccaa aggtccctcc ccagacatct ggacactggg catagatttc tcaagaagga     180

agactcccct gcctccccag ggcctctgct ctcctgggag acaaag                    226


<210> SEQ ID NO 30
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (216)..(216)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (226)..(226)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (255)..(256)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (261)..(261)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (284)..(284)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (313)..(313)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (328)..(328)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (333)..(334)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (356)..(356)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (411)..(411)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(471)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (473)..(473)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (492)..(492)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (497)..(500)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
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<221> NAME/KEY: misc_feature
<222> LOCATION: (503)..(503)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (510)..(511)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (513)..(513)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 30

ggccaccaga ggattctcag ggctcctttg tcctggactg tggaactggg ggcagctggt      60

ccctggggtc tctgaagtca gtgtctccct cactgctcac tgccatggtg tctctgcctc     120

tgcttctctg tgtccctcat cttcctccca cttcattctg actggcaagc cctgtcctgc     180

acagcttctt ccccnacccc taggccttcc ccaganactc cctctnacta ggctggctgt     240

tctgttccct tcccnnctaa nactgtggcc tggcccacct cccnaggaaa taggaaaggt     300

gcagaaatca ccntggagtt gccactcntg ccnnggcttc atctcgagcc aatgtnccca     360

ggtcactaag agaatgagct tccactgtat tcccatccag ggctctttcc ntttgtgagg     420

ctgacctgtg gacaagacaa tgggacaggg ataggcagtt cctccatcca ntntcataat     480

tgccaggcaa gntcttnnnn ccncctgcan nancctcccc agtggatcag gggttagaga     540

tattcaaggg tagtttcagg agcacag                                         567


<210> SEQ ID NO 31
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(97)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 31

taatgcggac gtaccgactg ccagatcttt acactcaccc ctccacctgc cccgaggagt      60

ccggtcacaa gggcccagcc antcacaaag acaccnnggt gtcccttcca ttttttttcca    120

cgaaggccca gaatccattt taggtttcca aacagacctt tcgtcccttc aaggtgtaac     180

caccgttttc cattccagcc attttattgg ccacaccgtt accttactta taggtatttc     240

cccagaagaa gactccagag aggaagctca tctgaggaaa gctgagaggg aagagaaacc     300

caaacatact gaagcaaaaa aaagcctatc cttcagaaaa aagcaacaaa aagatttctg     360

ttttatcttt cgaaactaaa actattggat ttgaagatta agtatcctaa acatcactga     420

ctagaaactg ttctctttgt cagcagtg                                        448


<210> SEQ ID NO 32
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 32

agtgtgcatg ttcactgggc atcttccctt cgaccccttt gcccacgtgg tgaccgctgg      60
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ggagctgtga gagtgtgagg ggcacgttcc agccgtctgg actctttctc tcctactgag       120

acgcagccta taggtccgca ngccagtcct cccaggaact gaaatagtga aatatgagtt       180

ggcgaggaag atcaacatat aggcctaggc caagaagaag tttacagcct cctgagctga       240

ttggggctat gcttgaaccc actgatgaag agcctaaaga agagaaacca cccactaaaa       300

gtcggaatcc tacacctgat cagaagagag aagatgatca gggtgcagct gagattcaag       360

tgcctgacct ggaagccgat ctccaggagc tatgtc                                396


<210> SEQ ID NO 33
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

cggtggcttg caacatgctc atgccagagc ccgctcaacg ctggctggtg ggcttcgtgt        60

tgtacacatt tctcatgggc ttcctgctgc ccgtgggggc tatctgcctg tgctacgtgc       120

tcatcattgc taagatgcgc atggtggccc tcaaggccgg ctggcagcag cgcaagcgct       180

cggagcgcaa gatcacctta atggtgatga tggtggtgat ggtgtttgtc atctgctgga       240

tgcctttcta cgtggtgcag ctggttaacg tgtttgctga gcaggacgac gccacggtga       300

gtcagctgtc ggtcatcctc ggctatgcca acagctgcgc caaccccatc ctctatggct       360

ttctctcaga caacttcaag cgctctttcc aacgcatcct atgcctcagc tggatggaca       420

acgccgcgga ggagccggtt gactattacg ccaccgcgct caagagccgt gcctacagtg       480

tgga                                                                    484


<210> SEQ ID NO 34
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

tctgacttcc agaacctacg ataatagact ccatgaaatc tgtaatcagt ggccacagga        60

aactcatgca acagcccttc caaggggctc cccagcaaag cctccgtggt gtctgccccc       120

aacccctgtg cctcctggga cacaagacag gcccagcaag ggtgggggtg ccacggaaag       180

cttggtggct gggcaggtcc ccagagggcc gccatcagtc ctcaaagaca tgctcagatg       240

cagtggctca ggcctggcac cagctggtcc caaggtgggg tggtgagggt acatctgctg       300

tgcacacgtg gctggacgcg ctgggggcag gtccaggtca gcttcaagga ctctgcccag       360

gctaacccta gaggcctcta gtgccagcag tta                                    393


<210> SEQ ID NO 35
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

aggcccatgt gctgtttttg acttcagtac ttcagattgc tgtgggaaca caggaggcag        60

cagccagatg agaaattgag tctgactctg gagtattata aagtccttat agttactggc       120

attaggtata gggtctgtat tattaaagag aaattattca ccaaacactt gttaaaaatg       180

gcaagacagt ttatttaaga gcattgcaat aggtaagtgc tatggtctca atgtttgtgt       240

ctccctcaaa ttcataagtt gaaacttcac ttccaagatg aaggaattag gaggtgggca       300
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ctttaaggga tgattatgtc ataggccaga gccctcatga acgagatcag tgcccttcta      360

aaagaggcat tgggagagac ccctcacctt ttccatcata tgaggacaca gccaggaagc      420

atcatccacg aaccagaaaa ttggcccctta ccagacactg aatctgctga tgtcctgacc    480

atggacttct gag                                                        493


<210> SEQ ID NO 36
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

acgctgcagc gtcacattaa tctttgtgcc gccagtgcct atgccatgct tagtatgcat       60

caaatatttg agcagtacac aagtgagtac tctgagagct cccccccacca aaaatatgat     120

gattaaatac agttatgatc agatccccag agtgtggctc taaactgtat gggggccaag      180

tttgaatact gttgtgtctt acactgttat tacctatcca gtatctattt ccccatattc      240

cttataaata aaacctagat tttgattggg acagtaaggt gtcccactga aaactcattt      300

ctctaaccaa tgtgatgcca gtgcttgccc aaaaag                                336


<210> SEQ ID NO 37
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

gtgagtgaac gtgaaggcct gcagcattac tgtacactac catagatttt tatcaacact       60

gtacacttag ggacactaaa cttatttaaa cattttttct tcaaaaataa attaacctca      120

gctcactgta actttataag ctttatattt aaaaaaactt tttgactctt ttgtagtaac      180

acttagctta aaacacaaac acattgtaca gttacacaaa atattttctt aaaaaatatt      240

ttattatatc ctattctata agcttttcct tgttttttcac tttttttttaa cttttaaact   300

ttttataaaa actaagacac aaacacacac attagtgcag gcctgcatag catcaggatc      360

atcagtatca ctgtctccca cctccgcatc ttgtcccact gaaaggtctt cagcgggaat      420

atcatgcatg gagctgtcat ctcctgtgat aacaatgcct tcttctggat acctcctgaa      480

ggacctggtt gagcctgttt tacagtt                                          507


<210> SEQ ID NO 38
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

gaatccctta agcagaacaa ccgtgatgcc atggaactca gcccaacgg cggtgctgac        60

caaaaatgtc tcaaagtcaa cagcccaata agaatgaaga atggaaatgg aaaagggtgg      120

ctgcgactca agaataatat gggagcccat gaggagaaaa aggaagactg gaataatgtc      180

actaaagctg agtcaatggg gctattgtct gaggacccca agagcagtga ttcagagaac      240

agtgtgacca aaaacccact aaggaaaaca gattcttgtg acagtggaat tacaaaaagt      300

gaccttcgtt tggataaggc tggggaggcc cgaagtccgc tagagcacag tcccatccag      360

gctgatgcca agcacccctt ttatcccatc cccgagcagg ccttacagac cacactgcag      420

gaa                                                                   423
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<210> SEQ ID NO 39
<211> LENGTH: 365
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (244)..(244)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (253)..(253)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 39

ttactctgtg attaacttcc ttctccctca ccccaaaata cagaagagtg aaatctctga      60

ccagaaagtt cctggcacct accttgggtt ctgtgaaaaa ataatggccc tggttttcaa     120

tgctgccaaa gttaagaaaa gttttcaccc cttcatttta aagcagccat aaagtgccat     180

gtgtttaacc gcaggaaaaa aagggtcttt ttaactattg agaagtagct tttcatatcc     240

ccancagggg aangaaagag cgggaaccag gagactcgtg aggactgcaa agatggtcct     300

ccctgggtac ttctgctgct ctcttctctc cagagctact ttgtgattgg cctgatggtc     360

agacc                                                               365


<210> SEQ ID NO 40
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

gatggagcat catgggttgg attattactg agttcaataa tctggtgggt tttgccagct      60

agaaacataa taaaatacat gataaaggaa tagaaaggaa atatatttat ttgaaattaa     120

attactgctt ataaattcat gtctctgatt ttacaaagtg taatgggtaa aattaccata     180

ttcttttttct tatttcaatc catacaatga gagtcatgtt cagttttttca ctgacttcat    240

gctgggtaat gttcactctg cattagcggt tgccatgttc accgttttct tacaatgtct     300

atccagtgct tgttactgtc tcactgacag acagaagtct agctgttttc atccacataa     360

tggcaggcag ggctagtgtt gctgctgct                                      389


<210> SEQ ID NO 41
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

ttatgtccct gctggtattt ttgctttttc ataaaaatta tcatttattt ttctcaactg      60

catattgcca tcttcatttt ttaatttct cacatattca tagaattgtt ctctgtaata     120

gatactgtac agtaattatt tgttgatcga ttaacctttt caatgctact tccgacacct     180

acttcccatc ctccgtgtaa cagatactgt cagttaccta tccttaacag cctttccact     240

cccaacttct gtgaatggac aagagatgca attgtgatca ctgaacatga ggcaacatct     300

tctaggaaga catttccata gtcttcagac aaaagggaga gatatctttt cagacaatct     360

ttgaacaatc ctatatgaag cttacctgaa gttgctgtag ccgtttggca agtctgggga     420

gactaacaga cacactgagg atagcagaaa ataaagatag aaacagccca ggttttttggt     480

gaaattcatg agcttctgaa taacgaaccc cataccaccc tacctctata aaagaat       537


<210> SEQ ID NO 42
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<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

tggatcccag catcgttggc aatagggttt taggtggagt ctatctggca ttcagagaag      60

agtcaggaaa acaattgtat tcccagcctg tgtccctagg gcacaagcaa atcccaaatt     120

ctcctcctga accctccaaa tttgtctaag aacttcgaaa actttaacaa acaggctgat     180

atcttcataa tattcccagc ctagaccaag caggaagaac attgatttca ttgaaataat     240

tgataataat gaagataatg ttttttatgat ttttatttga aaatttgcta attctttaaa     300

tggtttgttt tctacattga tggaattttt ctcttttaat ctatctacag c             351


<210> SEQ ID NO 43
<211> LENGTH: 528
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

tctgtttatc ccccaaatta ctacaaagca tagcgggctc tatgtttgct ctgttcgtaa      60

ctcagccact gggcaggaaa gctccacatc gttgacagtc aaagtctctg cttctacaag     120

aataggactt cttcctctcc ttaatccaac atagcagctg tgatgtcatt tctgtatttc     180

aggaagactg gcaggagatt tatggaaagg tctcttacaa ggactcttga atacaagctc     240

ctgataactt caagatcata ccactggact aagaactttc aaaattttaa tgaacaggct     300

gataccttca tgaaattcaa gacaaagaag aaaaatactc aatgttattg gactaaataa     360

tcaaaaggat aatgatttca taattttcta tttgaaaatg tgctgattct tggaatgttt     420

cattctccag atttatgaac attttttctt gagcaattgg taaagtatac ttttgtaaac     480

aaaaattgaa acatttcctt ttgctctcta tctgagtgcc ccagaatt               528


<210> SEQ ID NO 44
<211> LENGTH: 545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

gggacacacc agcacagtct ggtaggctac agcagcaagt ctctaaagaa aggctgagaa      60

cacccagaac aggagagttc aggtccagga tggccagcct gttccggtcc tatctgccag     120

caatctggct gctgctgagc caactcctta gagaaagcct agcagcagag ctgaggggat     180

gtggtccccg atttggaaaa cacttgctgt catattgccc catgcctgag aagacattca     240

ccaccacccc aggagggtgg ctgctggaat ctggacgtcc caaagaaatg gtgtcaacct     300

ccaacaacaa agatggacaa gccttaggta cgacatcaga attcattcct aatttgtcac     360

cagagctgaa gaaaccactg tctgaagggc agccatcatt gaagaaaata atactttccc     420

gcaaaaagag aagtggacgt cacagatttg atccattctg ttgtgaagta atttgtgacg     480

atggaacttc agttaaatta tgtacatagt agagtaatca tggactggac atctcatcca     540

ttctc                                                                545


<210> SEQ ID NO 45
<211> LENGTH: 166
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

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<222> LOCATION: (35)..(36)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(41)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(45)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(57)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 45

tgctgtttgt gtgaaacctc cactgtgcca agcannannn nannngactg tgaatanttt      60

aacatttatt cacagatagc atgaaaagcc acagtccatt tgccatttag cttatttgat     120

tgagagaaaa ctgaggcaca ggaaggcaca gtgactgagc aagagt                    166


<210> SEQ ID NO 46
<211> LENGTH: 205
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 46

ggatcagtct taagaggagc tttttttngg agcgagaaat catataaaat aaaatgaaat      60

aaaacaagga ggaaggcaac cagctgttag gggaaaaata aggcagataa aggagcgggg     120

agagaaatta attgccaacc aggaggagtt gggctgtatt tttcaaaggt ggggagagtg     180

gagcacacac cttgaggagg aaagc                                          205


<210> SEQ ID NO 47
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (132)..(132)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (193)..(193)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (207)..(207)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (213)..(213)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (219)..(220)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (242)..(242)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (260)..(260)
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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (267)..(267)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 47

gaaccatttg agattcaatg cctgtgtcca gctcccagga gtccaaccgt gaaatccaca      60

agtgcagncc ccaccctgtc ctgcagttct ctttcccttt a tgataatgtg gttgagtcct    120

ttgtcactcc cntcctcctg ctggctgcag aaatgacctc agcccaggcc agagacccca     180

gctctggcaa ggncctcttg tggtcgncca ggncccagnn tgaaagccaa gcagaatcag     240

gncaggatct ctagcgggan gggaaancct gataggacct ttgtcagact tttg           294


<210> SEQ ID NO 48
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

acatttaccg tattacctag cactttcatt ccttgttgtc tactccaaag gaaaaaaacc      60

tatgtccaca caacacatga atgtgaatat tagtagcagc tttatccata atagtccata     120

aagtagaaac acatcaaata tctatcagct gatgaaagaa taaacaaatg ggagtgatcc     180

atacaattta atagaatcta gcacctaaaa aaataaaata ttgatacgtg ctacaacaca     240

ggtgaaccac aaaagcacat taatctaagt gaaagaagac agatacaaaa aaccacatgt     300

tgtatgactc tattttttatg atatccagaa aagacaaatc tgtagtgtca gtaagtcaat    360

taggggttgt ctggagctgg ggagtgggaa taaggggtgg tattgatgag catgagggat     420

ttcttaggaa tt                                                          432


<210> SEQ ID NO 49
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (79)..(79)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (103)..(103)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (127)..(127)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (168)..(168)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (498)..(499)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 49

gtgaatccta gagtagtttg ctatcaactt ctgatctttg cacattctgg attnggcata      60
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taatgtnaca gcagtgccna ttgtaatgtt gcacaaagta gtntagcaat ttcttggttc        120

accaggntta gagataacat tgtagaaatg atccagcatc tttaacantc tgtggtttaa        180

ggtggggcac ttaggggtag aatcaataac aatgttagaa atcaaattag acaagataac        240

tgaaacagca tgatccatgt gtgactccaa gttataaagg aggacatgga ttaatggtat        300

acttctaggc tataggggta gtacaagtgg aaggacacca tcttagcatc agatcacttt        360

ctgagcaact ttggcaaatc ttttaaattc tctaatgtgt agtttttaa tatatgacac         420

aggtgtaaag aaaataaagc aagtgaatgt atgtgaaagc caatgctgac tgggcacggg        480

ggctcacgcc tgaaattnnt agcactttgg gaggcagagc cggggatatc acttgagccc        540

a                                                                        541
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<210> SEQ ID NO 50
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(69)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (88)..(88)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (285)..(285)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 50

tcatctacac gctggccagc aaggagatgc ggcgggcctt cttccgtctg gtctgcaact         60

gcntngnnng gggacggggg gcccgngncc tcacccatcc agcctgcgct cgacccaagc        120

agaagtaaat caagcagcag caacaatagc agccactctc cgaaggtcaa ggaagacctg        180

ccccacacag ncccctcatc ctgcatcatg gacaagaacg cagcacttca gaatgggatc        240

ttctgcaact gatcgtctcc atgcgccctg ctctgcggct gtgtncttat ttattgcatg        300

cgtcgcttcc acaggggccc ctcaagagct gtgactcggg agagctacct tactttgacc        360

aacagcctgc ccagtgtgga tgtctcttac aga                                     393
```

```
<210> SEQ ID NO 51
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

cctccttagc cttagaagcc agtggtgccc tgaccagagg ggaccctgtg ttcacaggca         60
```

-continued

```
tcctcaagga ttatcttcga gagttgccca ccccactcat cacccagccc ctgtataagg    120

tggtactgga ggccatggcc cgggaccccc caaacagagt tcccccacc actgagggca      180

cccgagggct cctcagctgc ctgccagatg tggaaagggc cacgctgacg cttctcctgg     240

accacctgcg cctcgtctcc tccttccatg cctacaaccg catgacccca cagaacttgg     300

ccgtgtgctt cgggcctgtg ctgctgccgg cacgccaggc gcccacaagg cctcgtgccc      360

gcagctccgg cccaggcctt gccagtgcag tggacttcaa gcaccacatc gaggtgctgc      420

actacctgct gcagtcttgg ccaggtgagt tcatgcccag ggcctgcacc accaatctga     480

gccaggctgc tacaatcccc gcctgccccg acaatctcca gatgtcgcgc cttacttgcg     540

acc                                                                  543


<210> SEQ ID NO 52
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

tcgcctgtac cagctggcat atgacaccta tcaggagttt aacccccaga cctccctctg     60

cttctcagag tctattccaa caccttccaa caggggtgaaa acgcagcaga aatctaacct    120

agagctgctc cgcatctccc tgctgctcat ccagtcatgg ctggagcccg tgcagctcct    180

caggagcgtc ttcgccaaca gcctggtgta tggcgcctcg gacagcaacg tctatcgcca    240

cctgaaggac ctagaggaag gcatccaaac gctgatgtgg aggctggaag atggcagccc    300

ccggactggg cagatcttca atcagtccta cagcaagttt gacacaaaat cgcacaacga    360

tgacgca                                                               367


<210> SEQ ID NO 53
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

cccccgagga caacctggag atcgttctgc acagatggga gaacaacagc tgtgttgaga    60

agaaggtcct tggagagaag actgggaatc caaagaagtt caagatcaac tatacggtgg    120

cgaacgaggc cacgctgctc gatactgact acgacaattt cctgtttctc tgcctacagg    180

acaccaccac ccccatccag agcatgatgt gccagtacct ggccagagtc ctggtggagg    240

acgatgagat catgcaggga ttcatcaggg ctttcaggcc cctgcccagg cacctatggt    300

acttgctgga cttgaaacag atggaagagc cgtgccgttt ctagctcacc tccgcctcca    360

ggaagaccag actcccaccc ttccacacct ccagagcagg gggacttcct cctgcccttt    420

caaagaataa ccacagctca gaagacgatg acgtggtcat ctgtgtcgcc                470


<210> SEQ ID NO 54
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

gtgtgtggat tcaacagtcg accccagctg tcgcagagcg cgaggaagct gcgcagtaaa    60

ccccttacat atcaacctct gaggaccggt ttttctgcac ctggtggtcc ttctagacgt    120

ctaggaggat cgtgttctca ggagagggtt cttcagcatc tgtgctgaag aacactgccc    180

cagcgggtca catgcaagat tccaccttcg agcaacatag ctgacactct gcagcccagt    240
```

```
tgtcacttgt aacaaacccc agtgggtcac atagtgaggg gaggcaaggc agcgtaaggc    300

agtggctgaa ctatcccaga aaacaaggat cacaggcccc cagtgacacc aatgttgcag    360

aaacacctgc agtggcaagt cagatgtcct ccaggaccag gcagataaca aggagtaggg    420

gtctgcagag gcctcgggag ggtctgcacc atccaaagaa atcaattgtt ctgcacagtg    480

gtaaggatcc agtgttccca gcac                                          504
```

```
<210> SEQ ID NO 55
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(66)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (70)..(70)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (345)..(345)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 55
```

```
gaacaccatt gtcttcaata acctgtnggg catatccagg aggcacatag ataggaggca     60

caganncatn tngggacatc attggaacct gagcaggacc tgtaatgcac tgaaactgtc    120

catcttctct tcttattgta aatgcttctc ctgggttaac ttgtaccaga ataacctgtt    180

gtgttccatc tgcacttaca ataggggcag acaaaagaga aatatcacta cttaagatct    240

gagttgtatc cagtagtggt ggatgttctg ccattatcaa taagacatta atatactgaa    300

taacgctcca attctccgag tcacgccgtt ctgaggcaga aggcngctcc tctggcgcct    360

cttcttaggg ttcctgatcg tt                                            382
```

```
<210> SEQ ID NO 56
<211> LENGTH: 440
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (83)..(83)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (262)..(262)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (373)..(373)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 56
```

```
gaagtgggag cggctcagca taggatgggc acgccatcag ccgtcaccag gcgcccggtg     60
```

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```
gtggggtcgt aggtgcccgc cangtagtag aggtcctgcc ggtcctggca cttgcggctc    120

cgggccatct gctcatactg ntcgcgcgcc acgacctggc acttgtggga gatggtctgc    180

acgtcgttct catcctcgtg gcaggactgg tacagcgcat tcttgccgtc gcactgcctc    240

ttgcccagct tggtctcctc angggtggta gaaccacttg accttgacca ccatgttgct    300

gccccacgac tcccacatgc tctcgatgcg gccgatgtag gggaggttgg gccgcccagc    360

tgacaggaag acngcacagt ccccgacacg cagggtctcc tcgccccgca cgatggcctt    420

gtagaacagc ttccgggcct                                                440
```

```
<210> SEQ ID NO 57
<211> LENGTH: 265
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

catcgcccac caaggcctgg gtgggtgaga acagtgccca caaggagacc ctgagtaaca     60

gagactcaca gcccatccag gtctctgggc aggaaattga aggaatcatc acattttaca    120

gaggaggaga ctgcagctca gagtggggga agtgtgtgca ccaggccaca ggcaagtctg    180

tccagagcac tggtaggaat gagggaaact aggaatgacc actttaaaaa gttagatgag    240

aagaatttca aggccgggcg cggtg                                          265
```

```
<210> SEQ ID NO 58
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 58

gctttatgca gtttgtcctt tcagttttca ggaatgagac ctcttgaccc ctcccctcca     60

atgcagcccc tactaagggg gagtttaagg agccatacat agttctataa ttcaaatcaa    120

gtaaacatgc ttcttgtccc aggttaactt gtgctgcctc agtcgctgtt taaacatttt    180

tatacgcact gttaacctgc ctgcccatta ccctattact tttaatggnt aaactactgt    240

tccctgggca gttgtctctt ttaacgtccc accctaaact tgccaaccct catatgaagg    300

cctcaggctt gttattggca aaggtcagaa gtcttaagct agtgaccttg caggc         355
```

```
<210> SEQ ID NO 59
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

ccctgacggc agaagagccc agcttcctgc agccctgag gcgacaggct ttcctgagga     60

gtgtgagtat gccagccgag acagcccaca tctcttcacc ccaccatgag ctccggcggc    120

cggtgctgca acgccagacg tccatcacac agaccatccg cagggggacc gccgactggt    180

ttggagtgag caaggacagt gacagcacc agaaatggca gcgcaagagc atccgtcact    240

gcagccagcg ctacgggaag ctgaagcccc aggtcctccg ggagctggac ctgcccagcc    300

aggacaacgt gtcgctgacc agcaccgaga cgccacccccc actctacgtg gggccatgcc    360

agctgggcat gcagaagatc atagaccccc tggcccgtgg ccgtgccttc cgtgtggcag    420

atgacactgc ggaaggcctg agt                                            443
```

-continued

```
<210> SEQ ID NO 60
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

gtctcgaggc agggctgaca catggtgcca tagccagcgg agggcgctca gtgagtgccc      60

cgggccttct agacaacagg caggaaggat gaacctcagg gcacccccag gtggtgcgga     120

aagccaggca gttgggacag aggtgcccac gagggcagag gccggtgcta aggggatggg     180

gaagaaggga caagattccc agagaggaga ggaggctgtt ggtaggaaag tggcagggct     240

gggggagacc cagccccaag ggtccggggc ggaggatgct ttgttctttt ctggttttgg     300

ttcctctttc gcggggggtg ggggaggtca acagggactg agtggggcag aggcccagaa     360

gtgccagcct ggggagccgt ttgggggcag ccccttctgc ccacccccatc cttcttcctc     420

tccagagatg ccaggggggc gtgtatgctc tgccccttcc ctcagacagg ggctgggtgg     480

ggaggctctt taggctcagg agaagcattt taaagaaacc cccaccctgc cgcccgcatt     540

ataaacacag ga                                                       552


<210> SEQ ID NO 61
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

ctctttatcc ctcagattac tccaaagcat aatgggctct atgcttgctc tgctcgtaac      60

tcagccactg gcgaggaaag ctccacatcc ttgacaatca gagtcattgc tcctccagga     120

ttaggaactt tttgctttca ataatccaag tagcagccct gatgtcattt ttgtatttca     180

ggaagactgg caggagattt atggaaaaga ctatgaaaag gactcttgaa tacaagttcc     240

tgataacttc aagatcatac cactggacta agaactttca aaattttgat gaacaggctg     300

ataccttcat gaaattcaag acaaagaaga aagaactcc atttcattgg actaaataac     360

a                                                                   361


<210> SEQ ID NO 62
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (33)..(33)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (69)..(69)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (77)..(77)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (91)..(91)
```

<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 62

caaagtggga ggattacaag tgttatccna ccnatgcntg gacaggaata ttttttaaata   60

atgaaaccna agttccnttt cgctttgtaa ngttaatgca tgtattgatg gtgagtagag   120

aacaatgaca caatctctag agagacatag gtgttcggcc tggctcaatc actagcctta   180

tagtctcaca ggaaaatatg aacttcatca aaatagctaa ttattaccac atcatgga   238

<210> SEQ ID NO 63
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

atgcagatga cgttgtggcc accgcactgg ccgtggagcc catgaagttt gtctacagag   60

gcaggatcgc tgtgttctct gtgaccgtgc tgcacgacga ccggattgtc ctggtggctg   120

agcagcggcc ggatgcctcg gaggaggaca gcttccagtg gatgagccgt gtgctgcagg   180

tgggcgcccc ggcacggcct atggttcggt gaatctccca agctggcacc cccactccac   240

tccaagtgcc aagtggttgg cttgtcccgc ccggtcctcc ctggctccag ctttgtttat   300

ctgtatttt cattgcaaat tgacaaatta cagctgtatg tatttacggg ataca   355

<210> SEQ ID NO 64
<211> LENGTH: 230
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

cctccctcaa agctactaaa catgaaaaca ttgtgcctat atgataaaaa tgtcaatatt   60

gctggtgata ctgatgctga tggaaatgac gatattagct gccattaacg tagtatctaa   120

tgtgtgccaa acaatattaa aaattgctgt atatacatgt ttgccattta ttatttataa   180

ccttaacaag atgtctcact cataagacta ctttccgcac tatgatacag   230

<210> SEQ ID NO 65
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

agtggcctta gacataactg ctgcccaagg agccacctgt gcccttttag gaacacaatg   60

ttgtacctta tccctgacaa tcagcagaac ataacagcag ccctgcaaag gggtcttcca   120

ggagattaag gtgactgaga gcctcactgt caaccccctg cagagatggt gagcatccct   180

aggttctggc gtacattggg ccctaatagt cataagtatc atagctgaga tcctagtagt   240

gagctgttgc tctctgtatt gttgttgtgg gttatggact cagggctccg ccatataggc   300

atgtgtccct gcctggagga cgccctcagc ctagggggtg tagtgtaagg gaaatggctg   360

tgctttagtc aggagtaggc tgaggcagcc ttctggtgca gcatgactca gtgggtttgg   420

agtgcaagca cacaaccttg ctcgttatgt aaccacacca catgaggccc attaggtaac   480

aactcacatg agctcgtgtt tggctcagag ccactattgt ctgtaaaagg tataccttgc   540

tgatgctgca ca   552

<210> SEQ ID NO 66
<211> LENGTH: 508

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (48)..(48)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (125)..(125)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (127)..(129)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (132)..(137)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (139)..(139)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (378)..(378)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (421)..(421)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (474)..(474)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 66

gggtgactgg tctaagtgct caattacctg tggcaaagga atgcagtncc gtgtnatcca      60

atgcatgcat aagatcacag gaagacatgg aaatgaatgt ttttcctcag aaaaacctgc     120

agcanannng cnnnnnnanc ttcaaccctg caatgagaaa attaatgtaa ataccataac     180

atcacccaga ctggctgctc tgactttcaa gtgcctggga gatcagtggc cagtgtactg     240

ccgagtgata cgtgaaaaga acctatgtca ggacatgcgg tggtatcagc gctgctgtga     300

aacatgcagg gacttctatg cccaaaagct gcagcagaag agttgacctc tagcaggctg     360

gctggatcac agctcttngc aattacatta tttataaaca cacacactag catgttttc      420

nagaccaaat attatcagat tacatataat ttaatcaaat taatttattt tttntgcctg     480

ccaaacatcc aatgtggtgc ttgttttg                                        508


<210> SEQ ID NO 67
<211> LENGTH: 410
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

gcatgtgtaa aaagtccttc agccacaaaa ccaacctgcg gtctcatgag agaatccaca      60

caggagaaaa gccttataca tgtccctttt gtaagacaag ctaccgccag tcatccacat     120

accaccgcca tatgaggact catgagaaaa ttaccctgcc aagtgttccc tccacaccag     180

aagcttccta agctgctggt ctgataatgt gtataaatat gtatgcaagt atgtatattc     240

ctatagtatt tatctactta ggatataaga tataatctcc tgattatgct ttcaatttat     300

tgtcttgctt cattaaaatg taaggctaag gagagcatgg aatttgtcag ttttgttcac     360
```

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```
taaagtattc caagtggttg ggaaagtgga acatttccaa gaaccaataa          410


<210> SEQ ID NO 68
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

cacaggatgt ggtctctacc gtgattcctg agcatgcatg caccccttct cctgccaata    60

gagggaggga agtcggaggg gtgtctttat gcctataaac ttgccttgga atccagcctc   120

actccctttc ctcctggagt tgagaagccc ccacagagac tggctatggg ggagtgactg   180

tctataggtt ccttggatgt cctgcctatc tgcaaaatga gaatgagatc gataccttca   240

tgaggctgta agatggcaga tataaaagtg ctgtgttatc tcaaaagggt g           291


<210> SEQ ID NO 69
<211> LENGTH: 326
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (218)..(219)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 69

actgtgtgca gcatattgca ggctttcact catttaatat ctacaangtc ctcaatangn    60

atatnaatta cttatgattt ccctgttttt tcttcctata aggaagctga ggcacaagtt   120

aatcaaagtc tcttggccta gggtgacaca gctaagattt gtacctagag atttctgagt   180

gttgacttct ctcctgcccc cacctatctc cccccccnna aaaaaaaaca caacaacaac   240

aacaacagaa cataccaggg attcatggct tgcccaatgt tggagggggga gaagagagga   300

gagggatgag ataagctcct cccacc                                        326


<210> SEQ ID NO 70
<211> LENGTH: 352
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (152)..(152)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 70
```

```
ttctgttttc ttcttaaagt catttatatt atgtattact cttaaagaat gttttagtct      60

ncattttagt agtctgtgca taaggtagta atacatgtac acaaagaaaa attcacaagn     120

cccattcagg tgtcttttag aacattattt anccactaaa tatttataca gttgacataa     180

tgcttattat gcccttgaat aatagaattt gttttgtttt tacttcttat ccataagcat     240

tggccttaca ttgcctcaag aggaacagaa tttattatta aacaggattc ttaaatccat     300

aactcatatt gtgacttcat acattttgta accctagtag tgaatatacc ct             352
```


```
<210> SEQ ID NO 71
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

gcccaaatcg cgcaggtctg ggacctgatt gcgggccacg aggcgcaatt cggggcggag      60

ctgctgctca ggctcttcac ggtgtaccccc agcaccaagg tctacttccc gcacctgagc    120

gcctgccagg acgcgacgca gctgctgagc cacgggcagc gcatgctggc ggctgtgggc    180

gcggcggtgc agcacgtgga caacctgcgc gccgcgctga gcccgctggc ggacctgcac    240

gcgctcgtgc tgcgcgtgga cccagccaac tttccgctgc taatccagtg tttccacgtc    300

gtgctggcct cccacctgca ggacgagttc accgtgcaaa tgcaagcggc gtgggacaag    360

ttcctgactg gtgtggccgt ggtgctgacc gaaaaatacc gctgagccct gtgc           414
```


```
<210> SEQ ID NO 72
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (138)..(138)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (208)..(208)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (213)..(213)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (220)..(220)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (242)..(242)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (251)..(251)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (258)..(258)
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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (281)..(281)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (286)..(286)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (357)..(357)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 72

tgccagctac aggtgctcac ctgaaaagca agccagacca tattaaccct nggcattgct        60

ggtacctngg aagactttct gattcaatgc tttccacctc ctcctacccc tcaccacccc       120

cgtnggcatg aaatcctngg gggctgcttt agaaattgtt ttctttggct gctggtgggg       180

gtgctgctgg tgggggtttg cacagctngg canactgcan ccagtctggt gggggtttgc       240

anagctggca nactgcancc agtctcctgc ctgctgccaa naaggnccat ttcccaagca       300

ctggctttgg agaagttggg gctctgaagt gggaacacaa ggctgccttt tgcaggncca       360

ggtgtaaatt ctccccctgc cactttcagc ctagcgtgaa acagatggag tgtgcattcc       420

cacttccctt tatggtaccc tggaatgatg gagctgccca gggcatcgcc acgttactct       480

ctagacagtc tctttgtctt cctgcaatgg cagcgccgag gttgtatatt tct             533


<210> SEQ ID NO 73
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (226)..(226)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (234)..(235)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (253)..(253)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (272)..(272)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 73

gaagggctgc cttattttag agcacagatt ttctgaatat ctattttgac aggttcgatc        60

ctctcccctt cctgccttcc ttctgtcgat tttcaatgtc ttgatggtgt cccacctgag       120

tggcctttag agatgtgagt tgtgaggcac tggggaggca ggcacacgtc ctccagccca       180

agactgccta atttaacagg gatttctgca ttctggaaca agcctnccat tttnnccca        240

agcaggatta ctnccagagg gcaaaacaca gncccaatag tatcacattt cctttctgct       300

ttagcaaaaa taaccactgt ctcattcatg ggaaaaggcc gccaaacaaa tttgttactg       360

gaaccatttg taacaacttc tagtttgcac tgccttggag caagcacact ttgtagagga       420

gggatttgca gttacttggg caacaaggta accactgatc attacaggaa gcttcagaaa       480

ccgtgggacc ag                                                           492


<210> SEQ ID NO 74
<211> LENGTH: 354
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (261)..(261)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 74

ctgttgctgc tgctgagcat gggcggggca tgggcatcca gggagccgct tcggccatgg       60

tgccacccca tcaatgccat cctggctgtn gagaaggagg gctgcccngt gtgcatcacc      120

gtcaacacca ccatctgtgc cggctactgc cccaccatga tgcgcgtgct gcaggcggtc      180

ctgccgcccc tgcctcaggt ggtgtgcacc taccgtgatg tgcgcttcga gtccatccgg      240

ctccctggct gcccgcgtgg ngtggacccc gtggtctcct tccctgtggc tctcagctgt      300

cgctgtggac cctgccgccg cagcacctct gactgtgggg gtcccaaaga ccac            354


<210> SEQ ID NO 75
<211> LENGTH: 275
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

agttccagaa atccagtgac gaatgtggta tacaaaaaaa tatataaatt ctttcaactt       60

agaataatta agtcataaaa tacatagggt acaaatacca cattccgttc taaaatgata      120

tcttaggatc atcaaaagaa aaagaggatt tggattatgc aaaaaatgat tcctatatat      180

ataatcaatt atctaactga catttttgca aatctaccac aacttcgcct tttattgcat      240

atgctaaaca agcagatgct aagtctgtaa actgt                                 275


<210> SEQ ID NO 76
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

ttgcttaatc atgcgctttg ttttttatgc attcacttcc tgtctttatc tctattttct       60

tt                                                                      62


<210> SEQ ID NO 77
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

ttaacctaag tatcagccct ggcatgctta tactggtcca agcaagcatt acgtcacagc       60

ctgttcctct tctttatcta aaagtgcttt ttcctttctc agcattccac aagttacttc      120

ctccttcctt tgttctcctc tgcctttgcc tcttttaaat agttccaagg tgctggccaa      180

tcgggacaaa tacagaatgt gaggtcccat tccagccctg gaaactggac acagcagtag      240

ggcggacgca tcaagtgata aatgaccctg tcccctttgt tcgctgtact ctcctggcaa      300

aactgctgga gagtgtaccc tttctgcaga aagtaaaaaa aaatggcctt gctgaggaaa      360
```

ttaatgttca agtgctattt ctttatggca ctggggaaca agcatttcaa acagacctga   420

ggtttacccg atttctgctg gaaaagaaac ctcaggtctg ctgccttaga a   471

<210> SEQ ID NO 78
<211> LENGTH: 373
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 78

tctgtaggag atcttccaaa ttactgctta tatacatgta tattctatta caaaaattac   60

accactcaat gtagtctaaa ttattgagag taaattgtag ccattctttt acatgttttc   120

tgaacttagt tgccaataat cataatcatt agctttttcaa ggtttgctct gaaacttaca   180

aaccatgcaa aagtgaaaac ttaggcttaa catatttggc aatttaaatc aactaaattg   240

aatcaatcta aatactgctt tgcaaagtaa aaaaggaatc aaaatgacac ataagacaat   300

cactaatccc tatatttta gggtctattt caagaaattt actactactt cttaccagcc   360

taaggactgt gta   373

<210> SEQ ID NO 79
<211> LENGTH: 505
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (334)..(334)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(471)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 79

aggccaggtg ctatgctcag agttcacacc tgcctgatac tgtgaggatt gggctacaga   60

ttctaaacca cactctccat agaggacatg gcaggtgagc ggctggcttc tgtgggtctg   120

ggcctggtgg gttagtgtgg gctgcatggc cccaaggctg ggagctgtgt tgggatctgg   180

tggcaggggg tttatctgac aacctcacta ttccatgtct cctctctgtg tggaggaatg   240

ggatgcagcg aggaggccag gctggagttc tgtagagtgt aaaatcctgg atgtcctctc   300

agcctgtctc cttgagagga cctgctgcct gccnttctgg agcacgtcat tctcttcttg   360

gatgaccaaa taaatcattc aagaatgaaa tgaaaactcc ttatctcctt ataggatctg   420

agctcagtga tgagaagtgg aaggacaata attgaccaat cacacattta natgaataaa   480

ttaggccgtt ggtgttcagc agcaa   505

<210> SEQ ID NO 80
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

tgtttccttt ccacttgcta gaagttattt tgccaatcac atatgattat tttatcattt   60

tttaattacc atcagtgcat gaaattatct ttattattca cttgttttta ttataatctt   120

ataatttcaa ataaaatgta aatctactgt cccttgcttt acctccgtgt cttcagtgcc   180

tagaacagga ctgtcataca cagtgactca atacacattt acttatgggt gattccctgc   240

ctgactgtta caggaagaag gaccaggaat atcagaatct gaagtgtcct ctaaagtcat   300

aaagactaga aggcattgaa taatgtttct taactatgca aggacttcag aattagatct   360

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cacata                                                                  366


<210> SEQ ID NO 81
<211> LENGTH: 455
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

agatctcatt ttctggaggt gcatgtctcc cgtgacccccc tctttggatt gcccgcagag      60

cccgtgaaga tggtgttatc actcctgtga ttactttact gatcaggtga ctttgagtca     120

atcaaaaggt agattatcca ggtgtgcctg atttgatcag gtggtccctt aaggaggctt     180

aaaatgaccc tttctgaagt agagtaattg gaaaagtaag agggtctatg ggtggggtca     240

cctggcaagg aactgaactc agcctccatg agctctggcc accagctgac ctttagcaag     300

aaagcaaatc tttctttggt cagtctccac aacaggacga agctggctga gcccttgcct     360

ttggccctgt gagatgctga cccgagtatc cagcgaacac gtgccagagt cctgacccat     420

ggaaactgag atgatgagtc tgtgttgctt taagc                                455


<210> SEQ ID NO 82
<211> LENGTH: 119
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

ccgattttct gtttgaagca gttcccttct atgttgcagt ctccttgaag gcaaaggttg      60

tgcactgtca tgttttgaag cccagtatcg ctgagaacaa tgacagacac atgcagtgg      119


<210> SEQ ID NO 83
<211> LENGTH: 137
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

tggctctcag agaaaccgta tttgatcaga gagctaaagg aagtgaggtt gtgagccaca      60

gggttatctt gaagaagagc attccaagga caggggaaac ttcctcaaag accagtaagc     120

cagagtgttc ttggtgc                                                    137


<210> SEQ ID NO 84
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 84

agcttacaca gcattcttag agaggacaca gaatttggag tttgagtctt gccaagttat      60

agggccttga gaaacattta gggctttcca tggatccacc ctaacgaagc ataaaattaa     120

gcctaggatt ttagggtcat cagccaaaaa tggaactgcc ttctagaaca aaaaatgaca     180

tccttttgag gaagacagtc atccagagtc tttacaatct tttacccaca ttgcctagta     240

cataattaaa catttctaga tatgaatagg aacaggaaaa tgtgacccat aatcaagaca     300

acaagcaata aatggaaacc tacccttaag tagctaaact gttgc                     345


<210> SEQ ID NO 85
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

<400> SEQUENCE: 85

tatgtttatt cagggctctg gaacataaaa aggctttgcc acactcttca catctataag   60

gtttctctcc agtatgaatt ttcttatgtt tactcaggta tgcagaccat ccaaaggctt   120

tgccacactc ttcacatttg taaggtttct ctccagtatg aattatctta tgtttattca   180

ggtctgtgga ccatccaaag gctttgccac actcttcaca tttgtggggc ctctctccag   240

tatgaattct cttatgttca ttaagggttg tgaaccgact aaaggctttt ccacattctt   300

cacatgtgta gggtttctct ccagtatgaa tactcttatg tttattaagg gttgcggatt   360

gtctaaaggc tttgccacat tgttcacatt tgtagggctt ctctccagta tgaattctct   420

tatgttcatt cagaactgag gacctactaa aggctttgc   459

<210> SEQ ID NO 86
<211> LENGTH: 229
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 86

gggagtggac ctgcattagc aagcagagaa tgtccagagc ctagagacag ccagcccatg   60

cagagggtag ggcataancc naggcagtgg agagggtgag gagtggtgta tagaagagag   120

catggagttt aaggggttat tatggctgag atccagacca tgagcagaga aaagttcagt   180

ttatctcacg gaaaacttta atgttaggct taatcctctg ttccttcct   229

<210> SEQ ID NO 87
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (80)..(80)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 87

ggttgatggt aatttatgta ccctgacagg ggtttggttt acatagctgt attcatttgt   60

caaaacttat attaaatggn tgcaattaat attgatgcat ttcattgtat gtaaatttta   120

ccctaaaata attttagaca aattgtaaaa cctagttaaa gacatatatg ctgatatttt   180

cagggttacc tctcttgatg tctgcaactt actttgaaat gcttcaaaag gaaaatagga   240

taatggatgg aaatagggag agagaaatgg atcgatgtgt aaataaaaca aatctatcta   300

aatgttaaag cttaattgta gatgatgaat gtaggagtgt tgaatgttaa a   351

<210> SEQ ID NO 88
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 88

aagagtctat gaagaaccca acggaagttt gtggcacatc cctaccctca aattcacagt   60

gagggtggaa tgcacagtaac caaatctgtg aaaatattca catgagacag gaaagaagtc   120

agaatatcca gtgtacaatg agagtgaaag aggatgtcta aaaggggaca gcccattcac   180

aacccacaca caacccacgc acaaatattt ttggggggggc ctcccatggg catttataat   240

cttctaagtg ctccgaagaa catgtgtcac aaaagatgaa gagaatattt tccagaacat   300

agcccaacaa agaacttctt tgacattttt tagtgtaaag gtaactgacg gtatctacca   360

aattagcaat ttgtaaaact ggaatttcta aaagcaaata cttggagctg agattacctc   420

ccacttccca aattcgagtt atatgatctc aagtataata ccctttggta tagacctagc   480

ca   482

<210> SEQ ID NO 89
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 89

tctgagtggg cctgctctct gtagactgaa ttcagca   37

<210> SEQ ID NO 90
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (130)..(130)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (135)..(135)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 90

tgcactcaat ggcttctgtt cgaagtccct attaaatgtt tctttcttaa atactgtatt   60

tgtcagcttc ttccttcagc atcccaactt cctcagactt tggggtactt ttgcacagac   120

ctagccaccn caaancactg tcatagatgc agcaatccac tttcacaaaa ccccatggac   180

aatgcagagg gggagaacag ggactgatta aagaaaggga cagaaatggc atcactatcc   240

aagactgaaa aacaggctga atggattatc actctgaccc aactgcacat ttctaatgtc   300

ttcatgtttt caattactcc atgaattccc ttatctgatg ctgattatgc acaggactgt   360

gtaagagtta aacaacacct gacactggtg actc   394

<210> SEQ ID NO 91
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (175)..(175)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 91

cctcatcact atgtcaccaa agtgttttgg aacttggtat tccagagact tctggaacgc   60

cgtgcaaggc ctgcccccag caagccacaa ccaggaaggt gcaggcacgc ccccactagc   120

tcctccccta tttattgcct cctggaaaac ccaggaccct cttccccatc tccanccct   180

acccctgggg gcagcccagg gagagccagg cacaatgagg gctcccaaca gctgcaagga   240

tttatctgaa cctttgagaa agaggaggag ccatctaagt ttctggaaac ctgagcccca   300

<210> SEQ ID NO 92
<211> LENGTH: 490
<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (69)..(69)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 92

cccattgcga tctggctctg ggggaccctg ggatgatatc cctaccccna gggacaggac      60

ccaaccccng gggacctgga gagactctgt gccctgcagg accgatgggg gactcctccc     120

tgtatgtacg tgtgcgtggc cctgccttgt tcttgccccg gacctggcct ggtgaaggag     180

gcacgaggaa gattgcagtc agggacgctc agcctgggag ctgaccctca ggtgaggccc     240

taaggaagtt cccagacctc cctgaacctc agtatgctca tctgtccagc agcaaccctg     300

ggccttaagt gagaacatct atgcggaaga ggcaggtgcc aatcaagccc tctgtaaagt     360

tacctcccct tttcccttct tctcctctca cagagctgaa gaatattttg caaagttcat     420

tgtaaacatt aaaataatct tgggtgttta tcattcgtta aacctgttgg gctgacttta     480

ggtctaccgc                                                           490


<210> SEQ ID NO 93
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

gagaaaagta gactccccaa tgcctcgcag taaatgagga cgcctggcgc ctgcggcgag      60

gtcaactgag gtcagacgag cttatctctc ctgtcccggg aattaagggc atcctgggga     120

cagctgcaga gcaggaggct ccccgtgccc tcctcttcct aagcaagtca ggatcccaag     180

aggcgcgtgc ggggaggccc ctccgaaggg ctgctggctt gtgtcttcca ccagcgcaaa     240

gggaagctat cggttgcttc tgcagtgagg caagctcagc cggacgccca gaagagagac     300

gaggtgtcgc tgtcggg                                                   317


<210> SEQ ID NO 94
<211> LENGTH: 208
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 94

atagatattt tttagtccac ttggctggat aataaantct taataacagg gggaaaaaaa      60

gaaagaaaaa ggaggaaaag atttaggaaa gaaaacaaca actttagtat ggaatgtgaa     120

gaactggcag gatattcacg ttgagctgtg cagtaagtag cttactggac atgtgaggct     180

gaagatacag ttgttcatat ggaagcaa                                       208


<210> SEQ ID NO 95
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

tccctcgtgt atcttatctt tattattgaa ttttccctca caatccactg ttaaaagaag      60
```

```
aaagtatcac acacgtgggt tcttttggct atggaagtgt ccttgagatc actttttgca        120

cgtgactcag ctgaagtgtt caaagcacat ggaaatcact tgccagtgac aggtggacgt        180

tgtatgtgtt ttctctctcc taaggatgcc taaactttct tttcttcaca ggtaaagtca        240

gtgataaatc ttttgtttgc tgcatatact ggagatgtgt ctgcacttcg aaggtatgtt        300

tacaggatgg attagcatgc actttacaga tatttatgaa gttgcttctg ggcgagcagc        360

c                                                                        361
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<210> SEQ ID NO 96
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (32)..(32)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (170)..(170)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (270)..(270)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 96

gaaacgccat ggaatgtatt gtatttctct antctatccc ttaaaatgnc cattgataat         60

tattggcaat ggttattgat agtctcaacg taatttcagt agaatttgtt ttgagatttt        120

ttttatgcac ataaaagatt tctttaggga ttattgtaca gagttctagn aaaatatata        180

attttttttt ctgggcttat aactttcttt tctaaaaatt tatttggcag cctgattaga        240

aatgtggtaa aatctgaaca ataaaatagn aaatagacta gttgcataga atgtttcaaa        300

aacaggcatt agattggcgg ctactcggga ggctgaggcg ggagaatcgc ttgagcctga        360

gaggtggagg ttgcggt                                                       377
```

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<210> SEQ ID NO 97
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (207)..(207)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 97

cacctttctg ttctgtgacg ggctgtccct gcttgtcctg ctttaggagg taggtaccca         60

gtggctcccc gncccctcag cggctcattc ctctcgctct ccccacgttg gtctgtgtga        120

gctccgctgt gtggctgcca ttcatccgat ccatctgtgg acttgctggg gctgcgccgt        180

gcacggtgtg gtgaatgcta canccanccc caggggcggg gctgagagtg gctgggacct        240
```

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ggagcacatg gggatgctgt gtgggaacca acttgccccc caccctgtgt ctctaggggt      300

ccgcagcagt agagaagcag acagccagcc ctgtccctgc ggcgtcaccc tccaccccat      360

actaacccag cagcgcatgg agagatttcg ggagtgctct aaaggccttt ggagcaattt      420

agggcaatta cggcagtttt tagaaatgct gaggggttgt tttgcctgcg gggcggggat      480

ggttgcctta tgcccacagt gaagcgggcg agatgcggta gctgg                     525
```

```
<210> SEQ ID NO 98
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 98

gaagttcaac tcaggaaggt gcaatataan caaatgtgct atattataat gaggaatggg       60

actaccgttc cagattttct gtaattgctt ctgcaaagta ataggcttct tgtccctttt      120

ttttctggca tgttatggaa tgatcattgt aaatcaggac catttatcaa gcagtacacc      180

aactcataag atcaaatttc attgaatggt ttgaggttgt agctctataa atagtagttt      240

ttaacatgcc tgtagtattg ctaactgcaa aaacatactc tttgtacaag aagtgcttct      300

aagaatttca ttgacattaa tgacactgta tacaataaat gtgtagtttc ttaatcgcac      360

tacctatgca acactgtgta ttaggtttat catcctcatg tatttttatg tgacctgtat      420

gtatattcta atct                                                        434
```

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<210> SEQ ID NO 99
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (202)..(202)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (386)..(386)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 99

gggagacaga tcacaatcag atccataagg aaaagtgtgt ctgtgtntat cttcctctct       60

agggaaaaat acagcagggt gaggggattg agtgggagtg caatcaggga agacttcctg      120

aaggcagtga ctggtgactg gaatgaagca tgagaatgag ccatgcaggt tgcccagaga      180

gagcatccag gcagagggag cngaaagttc catcctcacc cagctctgcc ggcccaggta      240

ctttctcctc tgccttctac tcccagtctc actccagtgc aacacacttc agttttctgg      300

gaactcctga tggaaagtgg ctgtatttgt tcatccctat agccttgggg cacagccagc      360

agccctgga ggaagccccg caggtnggta aagagacaca gggctcccag cc               412
```

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<210> SEQ ID NO 100
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 100
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actgttttca gacctaacct tggcaaggtc agtcctactt tgatgttctt gtttcatcac        60

acttcttggc atttgtagat ttggaagaat tgggcctttg gtacctctga tctcttcgtt       120

tagcaactta ctgtgcaccc atatgcttag cttttgctgt tttagctttt tttttttttt       180

tttttaacct gccacctagt ggccgaaatg ttgctatact attgataagg tactcctaat       240

tttggcaaaa tagtaagagg caaagcacca aagattatgt tctctccctt ctccaaatct       300

ctcttggtga gaatgatctt taaaacatac cactcagatt attagcaatc ttggtatgga       360

acgtttttaa aaataataat aatgtacttt atgtggtgat ttatgttatt atttaggccc       420

aaagttttga tttaattgtt tccttttagc ttattttttga gatatgcagt ctgttaggaa       480

gctgtctctg tct                                                          493


<210> SEQ ID NO 101
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 101

gccctcttgt gtagttttca ttgtgtctag tgcaatgccg taaaccttaa caccatgaga        60

cccatatgaa gtgccaacag tgatgatgga agcgctttca aagaaagaag tcatagacat       120

tataagaata aagcgacttg cttgatatgt acagtagata ggtacagctg tagctgctgg       180

ccatttcaga cagatgcttc atcttgtaaa cagcaacata aatgtatggt accaataaat       240

acagtacagt actgtaaatg tgtttttctct tccttatgat tttcttggta catgttcttt       300

tctctagttt actttattgt taagaatata ctatataata cacatacaaa atatgtgtta       360

ttgcctgttt atgttgtggg tagggcttct ggtcaacagt gggctacatt atcga           415


<210> SEQ ID NO 102
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 102

ggactagcag tcttcttctt cagacgccat gggacccca ggcgactgct ctactgccag         60

cgttccctgc tggacaaggt ctgacgccca ccgccggccc gcccactcct accacaagga       120

ctttgcctct gaagaccagt gtcagcaagg tggtggtggg tgggctgctc ccatccgtcc       180

ggagccccct ccccgcagcc tccttgcttc tctcagtccc ctggctggcc tccttcacccc      240

tcaccgcctg tagcttgtgt ctgtccagcc ccatctgaat gtgttggggg ctctgcactt       300

gaaggcagga ccctcagacc tcgctggtaa aggtcaaatg gggtcatctg ctcctttttcc      360

atcccctgac ataccttaac ctctgaactc tgacctcagg aggctctggg cactccagcc       420

ctgaaagccc caagtgtacc cagttggcag cctcccgtca ctctgactaa aaagaatctt       480

cagagtgcat atttggaggt ggaaagattg ttcagttacc ctaaagactt                 530


<210> SEQ ID NO 103
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(48)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(53)
```

```
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(59)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(85)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (117)..(117)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (125)..(125)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (179)..(179)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (266)..(266)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (272)..(272)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (277)..(277)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (285)..(285)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (359)..(359)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (467)..(467)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 103

taatttttagc tccaatccat ctttctcttc tccaaaaccc tacctcnntn nnntcnnnnc      60

cacccctttaa gtacttagtc atgcntagcc ttatattctt gtttgaattc tnatgtnctg     120

nnccncccaa acagattata catttcttgg gtcccatact ttgcatttac catagcagnt     180

ttcatagccc atacaaacat taggccttca aaatatttgt caagtatttc ttcaataaaa     240

atgaaaacat cccaaatctt gatccnccta anatgtnaaa tgggnactta gttaagcaaa     300

ctaacatcat gatatactgg aaacaggtat ctctttcctt taccccttgtg cctgctgang     360

atcttattct cagccttgct gttttaaact caggggtgtg tgtacaacat atttaagcaa     420

attctggaat accaaagcca agcagtcttc caggggcttc atcctgncac acagcagctt     480

acctggtggg tgttgggtag cacacagta                                      509


<210> SEQ ID NO 104
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 104

catgatcagt gtattttagg gggactaata tggcaactaa agctactttg gaagagaaag      60

agtggagata catagattgc tattatagtt caggccaata gagaggaatt gggtttaaga     120

gatacattat ggaggcagaa gtgttcattc aacaagcgtt tgttaaatat ctactatgta     180

atcatgatta tacaactaga gagaatatga aaaaaatgaa ttacgtatgt tagcttatag     240

atggatgctc tcagtaccca tccctattaa tcgtcatttc cctttgttta gtgaaccttc     300

tgatatattg gatatcaaat atcctttcca agtattgt                             338


<210> SEQ ID NO 105
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(35)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (241)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 105

gttccaggtc ccggatagcg agggcngccg cgcnngctcc nagggccatg aagcccccag      60

gaggagaatc gagcaatctt tttggaagtc cagaagaagc tactccttcc agcaggccta     120

ataggatggc atctaatatt tttggaccaa cagaagaacc tcagaacata cccaagagga     180

caaatccccc aggatcatgt tttcttatgt gaaggagaag aaccaaaatc ggatcttnaa     240

ngcttgcaag gagcatcccg gctgggagca gagccaggg                           279


<210> SEQ ID NO 106
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

ccaggctact gctaagactc gtacttccca gtttggtgtg ggcagctttc agactccatc      60

ctccttcagc tccatgtccc tccctggtgc cccaactgca tcgcctggtg ctgctgccta     120

ccctagtctc accaatcgtg gatctaactt tgctcctgag actggacaga ctgcaggaca     180

attccagaca cggacagcag agggtgtggg tgtctggcca cagtggcagg gccagcagcc     240

tcatcatcgt tcaagttcta gtgagcaaca tgttcaacaa ccgccagcac agcaacctgg     300

ccagcctgag gtcttccagg agatgctgtc catgctggga gatcagagca acagctacaa     360

caatgaagaa ttccctgatc taactatgtt tcccc                               395


<210> SEQ ID NO 107
<211> LENGTH: 412
<212> TYPE: DNA
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

acatagagag gtgactcatt cttttttaaag gttacattaa gtttgtagta tgtcagaatg   60

gcaatactat aattgtttta accagtgacg tttaagttgt ttccagagttt tttgatctaa   120

caaataatgt gtcatgagta tagaattttt atgttcatgt actagtatag ttataggatg   180

actcatatttt gaagcaaagt acaaaacgca tgctttctgt agctactcat aaattctggt   240

atgagcaaaa tgtcaagatg cttgcttatc accgaccaag tgatgattaa gctcttgcta   300

aactgtatca aaggagaaaa agggaaatac aggcttatcc taacaatttc acagtgaaca   360

gtaatctctg gcattcagtt aaagctagac ttgttctaat tactttgatt tt   412

<210> SEQ ID NO 108
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (248)..(248)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 108

gtaagtggta ccagccacaa ctgaatatcc atctgggata aaataaaatt gcactcgtct   60

tagagatcca aatcaacttc agatggatta aaactttgaa tgtaaaaaac ataaatgact   120

nacagtcctg caaaatatct tggagacaac ctgtgccatc tggagagtgg gaagagcaca   180

tgcaaaggcc aaggggtgga gcagcccagc atgttctgga aaaggtaggg ctccccaagg   240

ctgggatnat ggtggagacc tgggtgtgtg ggagcacagg ggtgggggcc cgtgggccag   300

gaatgcacag agaggggctg gtgctctgcc gcaggcccaa gccccaaag cccggtcatt   360

cccagcacca tcttcacggg tttctgccca ggtctttctg ctgcatctct tcctcccccg   420

attccttaat cattttttttt aaaatcagtt catgtctttg taaaccaaat tatttctaaa   480

aggcaaattt atattactgc cgaaatcaag ggtcagtgag ctagttgtgt a   531

<210> SEQ ID NO 109
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (98)..(98)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 109

gacttgggat tccggagcag tcgcccctat cgctgctcct gcagttgcgg acnccaccga   60

ccccgccgcc ggaggactgg gcactgaaag gcctctangc ctaggcgcgg cccgcggagc   120

cagacgtgtt gctgccgtga gtaaaacgag cgccctctcc gcactcgttt acaaattaaa   180

atggaggaaa tttcgttggc caacctggat actaacaagc tagaggccat cgctcaggag   240

atttacgtag acctgataga ggattcttgt ttgggattct gctttgaggt gcaccgggca   300

gtcaagtgtg gctacttcta cctggagttc gcagagactg gtagcgtgaa ggattttggc   360

```
attcagccag tggaagacaa aggagcgtgc cgcctcccgc tttgctccct tcccggagaa        420

cctgggaatg ggcctgatca gcagctccag cgctcacctc cggaattcca gtagctgcaa        480

aatgagagtc tgaaagtggc caggacaata acatagactg gtcctgtggc ttcgaggagt        540

a                                                                        541


<210> SEQ ID NO 110
<211> LENGTH: 359
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 110

ctccctgcaa atgcacatgt caatcaatga ttaatgcacc caggttatgt acaaggcact         60

gggcttagca ccacagggaa cttccttcca gaggctcgct ttctagttgt gtagacaaga        120

atacatgcat gagaagatac aagacaattc acccatgcca aatgattcat acaggctgtt        180

taagtactgc agaaaataaa agaaggaaag gctaccagac ttttcaataa ggtctacagc        240

ttcccaagag catgtctttg ttaaatcagg aaatataaaa attatgtgtg tatgtgtatg        300

tatatatata taccacccta ttaactattt taaaatcgta ttctattttg ggggttgtg        359


<210> SEQ ID NO 111
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(56)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (151)..(151)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 111

cagagtggac tgttccctga ggtgggagat gtggaaaagc caagaggctg cagccnaggc         60

cactggcccc tgagatctct gcaggaaatg gctgtggagt gtggcagttt ggcaaactct        120

ccaccacacg taatgaaact tggatttgct ncagtgtctg gctgcagagc agtgggcctg        180

gccagcaggt ccccagcttt ggctatgagg gccttgagtc ccccaaaaca ccgggttcca        240

gcaccacact cagccctcat tggctcttga actgagcttg gaagcttctg gtgaccttcc        300

aagagcctga gagtgaggtg gaattatttt aaaagataaa tattatatta tatatatata        360

tatttccctg aaggaaccaa agcgaatttt aaaagatgca atgtagaggg gaaaagagat        420

gatgaaaata tttaaaggcc ctatctgttt acagtgttcc gtggttaaac tcgctcactg        480

ctaagaatat t                                                            491


<210> SEQ ID NO 112
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 112

gtgatcatga gaatgctgcc tttaaagatg tggccctggt cctgactgtt ctgctagagg         60

aggaaacatt agaagcaagt gtaggcccaa gggaaacgga agaaaaagtg agagacttac        120

tctgggccaa gtttaccaac tctgacactc ccacctcctt caaccacatg gactcagaca        180

aattgagtgg gctgtggagc cgaatttcac acctggtact gccagtccag ccaatcttag        240
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atgctagcgt tacatccaca aaaccagtgt tgccttgtat aactatt                   287


<210> SEQ ID NO 113
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

tagccgatcg ttacctcaag ggagtgggaa ttgggcccag ctccggcccc tcctggtcac      60

ctttggccat gatggccggg gccatgcctt gacccgacgc cggagggcca agcgtagccc     120

taagcatcac tcacagcggg ccaggaagaa gaataagaac tgccggcgcc actcgctcta     180

tgtggacttc agcgatgtgg gctggaatga ctggattgtg gccccaccag gctaccaggc     240

cttctactgc catggggact gcccctttcc actggctgac cacctcaact caaccaacca     300

tgccattgtg cagaccctgg tcaattctgt caattccagt atccccaaag cctgttgtgt     360

gcccactgaa ctgagtgcca tctccatgc                                      389


<210> SEQ ID NO 114
<211> LENGTH: 499
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

gtacctcgct ggacctggag ttagacctgc aggcgacaag aacctggcac agccaactga      60

cccaggagat ctcggtgctg aaggagctca aggagcagct ggaacaagcc aagagccacg     120

gggagaagga gctgccacag tggttgcgtg aggacgagcg tttccgcctg ctgctgagga     180

tgctggagaa gcggatggac cgagcggagc acaagggtga gcttcagaca gacaagatga     240

tgagggcagc tgccaaggat gtgcacaggc tccgaggcca gagctgtaag gaacccccag     300

aagttcagtc tttcagggag aagatggcat ttttcacccg gcctcggatg aatatcccag     360

ctctctctgc agatgacgtc taatcgccag aaaagtattt cctttgttcc actgaccagg     420

ctgtgaacat tgactgtggc taaagttatt tatgtggtgt tatatgaagg tactgagtca     480

caagtcctct agtgctctt                                                 499


<210> SEQ ID NO 115
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

gagtttcagg accaggcagc ttgattacag catcaagggc ccctgtgttc tctgttttct      60

gcagccatag tattggcttc ttcccaagac ttatttttcc catcagtgtc acctgtgcta     120

caagctcctt cagtcacatc tatttttgat atttgtgggt acctaggagg tgcatatatt     180

tgtgggatac atgagatact ctgacacaga tgtgcagtgt gcacggatca cagggaaatg     240

gggcagccat ccatcccttc aagcattcat gatttctttg tgttgtgaac attcccgttg     300

tgctctctta gttattctga atgtacaaga aattattgct gactatagtc accctgtcgt     360

gctatcaaat actagacctc attcgtggta tctaactata ttttgtaccc attaaccatc     420

cccatctccc accccctacc tttcccacta tccatcccag cctctggtaa ccatccttcg     480

tctatctcca cgagttcaat tgaa                                           504


<210> SEQ ID NO 116
<211> LENGTH: 476
```

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (423)..(423)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 116

agcacagtct ggctggatga gacagggtcg tgcccagatg atggagaaat cgacccagaa     60

gcctgaggag gtgtcctggg tttggctggc tggctcctgc tccagcggcc cggcttcagg    120

tgtccggggg cgtggctgcc tggagcaggt gtgctgaata ccctggatgg gaactgagcg    180

aacccgggcc tccgctcaga gagacgtggc aggaccagcg aggaatccag cctgtccact    240

tccagaacag tgtttcccag gccccgctga gtggaccgga cctctgacac ctccaggttc    300

ttgctgactc cggcctggtg aaagggagcg ccatggtcct ggctgttggg gtcccaggga    360

gaggctctct tctggacaaa cacaccctcc cagcccccag ggctgtgcaa acacatgccc    420

ctnccataag caccaacaag aacttcttgc aggtggagtg gctgtttttt ataagt        476


<210> SEQ ID NO 117
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

atccttgtac ctgatgtctg agccactcag aactcaccaa aatgttcaac accataacaa     60

cagctgctca aactgtaaac aaggaaaaca agttgatgac ttcacactgt ggacagtttt    120

tcccaagatg tcagaataag actccccatc atgatgaggc tctcacccct cttagctgtc    180

cttgcttgtg cctgcctctt tcacttggca ggataatgca gtcattagaa tttcacatgt    240

agtataggag cttctgaggg taacaacaga gtgtcagata tgtcatctca acctcaaact    300

tttacataac atctcaggag gaaatgtggc tctctccatc ttgcatacag ggctcccaat    360

agaaatgaac acagagatat tgcctgtgtg tttgcagaga agatggtttc tataaagagt    420

aggaaagctg aaattatagt agagtcccct ttaaatgcac attgtgtgga tggctctcac    480

catttcctaa gaga                                                      494


<210> SEQ ID NO 118
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (235)..(235)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 118

gataacccca atctacgaag actagctatg gaacttccta cactgagaca actccagtgg     60

aactctgata attatcctaa aataaggagg cttcttcagt agccctcgaa atatgttcaa    120

atacatgatt acatttatgt ccttaatatt gctattagtt tctgatgtta atgtaaaagt    180

tggggaaaaa ngtggaaaag ttaaagcagt gcaggttaat tcaatgccag agtancttct    240

cagagggtgt atattcagtg tgaacaattt tcaacagaga aatgtcaact tctggccaca    300

acggcaacca gtaaaatgac tattttact gtcttatcta ttaatgaaga ggagattgca    360
```

```
taatatagat gaaggagcat agtatttgca ggtggaacgc ctagcagggc ttgagtctca      420

actctgctgc ttttactcta attgaccgag acaagtcatt taaactaata gagcttcaat      480

tttctcatat ctaatgtaac ataacaattc acagcctttt actttgtagt tatcgtgaag      540

atctaatcgc agt                                                         553


<210> SEQ ID NO 119
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

ctcctgttca tcctgttcac agagtggctc ggctgatggt agctcgacca atggctgcaa       60

ccatgagagg gctcccctga aacttctctg tgacaatatg aagtaccaga tcctctccag      120

agccttctat ggatggctgg cctactgcag acacctgtcc accgtgagaa cccacctatc      180

agccctggtc aatcacatga tcgtgtctcc agacttgccc tgcgatgctg acagggact       240

gacagccagg atctgggagc agtaccttca cgacagcaca agttacgagg agcaggagct      300

gctgcgcctc atctactacg ggggcatcca gcctgagatc cgcaaggccg tgtggccctt      360

cctcctgggc cactaccagt tcgggatgac ggaaacagaa aggaaagagg tggacgagca      420

gattcatgcc tgctatgcac agaccatggc tgagtggctg gg                         462


<210> SEQ ID NO 120
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(56)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 120

tctgctgctg aaggcctgtg attttgtngg ggaagggcct gttctangca actggnaaag       60

gcactgccac ctgccgttgg atgccaggac tcaagagctg gccccagtca ctgtgcgcag      120

agctgtctga gaatgtgtga gtggactggg tccttcggca ctgcctgcat ggctcaggg       180

cagtcaaccg tcgcagagga tgaggggcac actcaggcag cctccccggc cctggaggca      240

gaaaggccca ggcagaacca ctgactggga ggaaacagaa aaagcagagg agagccaggc      300

tgcaggcgtg tggatgggac cagctcaggc agacgctgtc tcatacccac tctcccctct      360

cttgccaggg cctggcctgg tgtctctcag gagcctgggc atgagacaaa agcagagatt      420

gttctcttgt ggtaccacag gctgtaacca gtccacccag tgttgtttta gaaatttaaa      480

tcggttgccc atcttttta attggcaaca tcgtttacca catt                        524


<210> SEQ ID NO 121
<211> LENGTH: 326
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

ccccaagttg gcgggcctga ttgggcggca cgggcccag aacaagcagc ccttcatggt        60
```

-continued

```
ggctttcttc aaggccacgg aggtccactt ccgcagcatc cggtccacgg ggagcaaaca    120

gcgcagccag aaccgctcca agacgcccaa gaaccaggaa gccctgcgga tggccaacgt    180

ggcagagaac agcagcagcg accagaggca ggcctgtaag aagcacgagc tgtatgtcag    240

cttccgagac ctgggctggc aggactggat catcgcgcct gaaggctacg ccgcctacta    300

ctgtgagggg gagtgtgcct cccctc                                         326


<210> SEQ ID NO 122
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 122

atgcggagtg agaaaagcct gttgcagaag actacataca acaggatttg acacttgtaa     60

ggctccaaaa caaagaaaat aaatgatat tgtttaggtt ttcatacata ggtgataaaa    120

gtgtgtttct ttgtttttaa tgagaaaatt agtcacagaa tttaagatct tagttacttc    180

tatagggaag gcaggggaat gggacaagga ggaagcccac agcattggtc atgctctcat    240

gttgaagttg ggttcaaagg tgttcattat taaaatgctt cataatgatg accatacatt    300

tggtatttct aggacaatct tggtttacat ctattgtctc aacataatta ttcagtgcaa    360

gcctttcctt tc                                                        372


<210> SEQ ID NO 123
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

ctaccttgcc tgctgagaca tagggctcca cgggtctctc tcctggggcc gggctgactg     60

tggcctgcga ggggcagtca tcgtgttggg ttttcctgcc agaggcagaa accacaaaat    120

tacctggaac atacacgccc caagtgacag attcaattca attccacaaa tattgacctc    180

gcgtctaatc cactcgt                                                   197


<210> SEQ ID NO 124
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

ctctgagcct tgcttggttg tcagaggcca tgagaggtgc cagttatagg tggatgtgcc     60

aagatgctgg tgaacttggt cttcagctat acccaggctc agaaagggca agagccatgc    120

tgcagcgtag gtgactttgg aggtgcactt ggggcccagg gctttgagtg ttgcgggtgt    180

gcctgtccct ccagatagtg ctctgtttct ctctgttgtc ccctgcctg gtcctctggg    240

gccactgtgc tttctgctgt gtgcatttat aaatgatgtg tattttatat agacctgctt    300

gcattggctg atgctcctct aattccctga gtttgattca accacccttg ggttgttttg    360

ctatggcctt agcctttga                                                 379


<210> SEQ ID NO 125
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125
```

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```
gaaccagaat ccttggaagc tctaggtcct acctcagaaa atctcatcgt catggttctg        60

cttcaagaac agaatttggg aattaggtat aagttcaatg ttcccatcac tcgaactggc       120

agtggagata atgaagttgg ctttacatgg aatcatcagc cttggtcaga atgctcagct       180

acttgtgctg gaggtaagat gcccactagg cagcccaccc agagggcaag atggagaaca       240

aaacacattc tgagctatgc tttgtgtttg ttaaaaaagc taattggaaa catttcttgc       300

aggtttgctt caagctgtaa tttagcaaaa gaaactttgc tttaattata ttatattcca       360

tttgttttca acctcatgta atttgtgcag atttgttggt aaaatacatc ttggcacaat       420

gagtgtctct gctggtgctt ctcccaagac tatcttgaag gtgggctgtt tgcctttcgt       480

gaacacattc ttggt                                                         495
```

```
<210> SEQ ID NO 126
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

atacctcatg cagccttcag gttcagttct gacaccaggg atggaccatc ccatttctct        60

ccagcctgcc tccatgatgg gacccctac ccagcaactg ggccatctct ccctcagcag       120

cacaggcacg tatatgccga cggctgcagc tatgcaagga gcttacatct cccagtacac       180

ccctgtgcct tcttccagtg tttcagtcga ggagagcagc ggccaacaga accaagtggc       240

agtggacgca ccctcagagc atggggtcta ttctttccag ttcaacaagt aacagtggga       300

ttcccctccc catctttact gaatagaaat gaattcttgg agatactcat gctcccagat       360

tccagagggt taaccaggaa tggagaccat ccgtcggccc tgctaaggac taacacttag       420

ccatcgtttt tcacaggcct gggcctggaa aaagaaatct ctacgttcct gcccttact        480

attgctgatg g                                                             491
```

```
<210> SEQ ID NO 127
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

ggtgctgccc tgtgtacata taaatgaatc tggtgttggg gaaaccttca tctgaaaccc        60

acagatgtct ctggggcaga tccccactgt cctaccagtt gccctagccc agactctgag       120

ctgctcaccg gagtcattgg gaaggaaaag tggagaaatg gcaagtctag agtctcagaa       180

actcccctgg gggtttcacc tgggccctgg aggaattcag ctcagcttct tcctaggtcc       240

aagcccccca cacctttcc ccaaccacag agaacaagag tttgttctgt tctgggggac       300

agagaaggcg cttcccaact tcatactggc aggagggtga ggaggttcac tgagctcccc       360

agatctccca ctgcggggag acagaagcct g                                       391
```

```
<210> SEQ ID NO 128
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

tgtatggtcg ctggccagtg attctccttc tgagccgtgt ttcccctctc cctccctctc        60

cacgtgggca gggcaggccc catcgctttc ctctgataac cacatggaca catcctgaag       120

tcagcccagg cgccctgagc atcttggggc acctggaccc catcacaata ctccttcttc       180
```

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```
cttcaggtcc ctgggtgaag gctttgctga aaccgacccc cctttttcacg tcccttctgc      240

ctctgccccg ttggatgccc tgactggggg caggggaaga gacagggcac agctggccac      300

agggctcagc cactgagcag gctgttccgg gcctttggct ttgcatcctg gacggggagt      360

gtcctgtcag ggaccagatg tgtcctgcct catccctagc tccaatccct tccccacgtg      420

accggggatt ctggttgcaa taaaacatgc tgctgctg                               458


<210> SEQ ID NO 129
<211> LENGTH: 496
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

gcagtctcgt ccaatttcta tagcaccgtg ggcaggaacg gcgtcctgcc acaggctttc       60

gaccagtttt tcgagacagc ctacggcacc ccggaaaacc tcgcctcctc cgactacccc      120

ggggacaaga gcgccgagaa gggggccccg gcggccacgg cgacctccgc ggcggcggcg      180

gcggctgcaa cgggcgcgcc ggcaacttca agttcggaca gcggcggcgg cggcggctgc      240

cgggagacgg cggcggcagc agaggagaaa gagcggcggc ggcgccccga gagcagcagc      300

agccccgagt cgtcttccgg ccacactgag gacaaggccg gcggctccag tggccaacgc      360

acccgcaaaa agcgctgccc ctataccaag taccagatcc gagagctgga acgggagttc      420

ttcttcagcg tctacattaa caaagagaag cgcctgcaac tgtcccgcat gctcaacctc      480

actgatcgtc aagtca                                                       496


<210> SEQ ID NO 130
<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (475)..(475)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 130

aggtcaccca gctgtgaatg aacgtggtca gaacacagaa tctgagttgg tcacacttcc       60

cactgatcca tggggccttt aagccctctg gaagcttcca ttaaagatga ttatttgagg      120

ataattgtat tgggatgcct atgatcttat ctagggtttt cctacccatc cccaacattc      180

agctcagctg cctctttctt gaggacaccc tcactgatca ccccagccca gccagagtgg      240

ttgctcctgc tcctgcccct gaacctatga catacccaag tcccaatact ttcgagccat      300

ctgccactgc cttttgacat ctctgccttg gctagattca aatggtgttt cataataaaa      360

gtctgagttt aagcagcttt accgaaaacg caagggaagt tcattccat ttatacttct       420

ccagaccccc tgccatcctc tgctgctacc cacacaggca gaataaaagg cttanatgtg      480

taagtcccat gaaggcaaag attggtctct tgtgttcact gctgtctgta gtacttag       538


<210> SEQ ID NO 131
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 131

gtggcaaaag gggattcggc agctgtgatt aagaaccttg tgatggggag ggattcctgg       60

attacccagg tgagtttaat gtaaccacaa agatcctttc aagagggagg caggaaggtc      120
```

-continued

```
tgaggcagac gaaagagctg tgccaaggga agcaggcggc agtgggatgc aggtggcctc        180

tagaagctgg aaaaggcaag tccatgggtt ctttcctgga gccttcagaa ggagcacggc        240

cttgctgacc catcttagaa cggcaggata atcaatgtgt gttgtttgag gccactaagt        300

ttgtggcaat ttgttacagc agcaatagga aactactaca ctgtgtctga ttagatcagg        360

ccaatgaatg gagaaagtat tggatttcag ttgagtgcta aaacctggtc tgtt             414
```

<210> SEQ ID NO 132
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

```
ccagcttcac atggtctctc aagtgcttat gcttttcttc tctctgccac ccacattccc         60

acatcccgcc caccccccaa ctttcctccc ttcaccttcc catggagact ttttgcctgg        120

gctaaatctg atcctcagcc cactctcaga atcgataaat gcccctaggt gattgtaagc        180

tcacctaaga tatacttttt ctcctctaga attttagttt attagatttt tctagttgtc        240

tttgcaaaag cgttaacagg ctctgacttc tgacattcaa ctagatgtgg aatatccaac        300

ccctagcatt tcatggaatg tactgaccaa gataaaatgt gttcttatta aacaatgcca        360

tttcttgacc acttctgttt ttaggaattg tggtatctga gtcatggt                    408
```

<210> SEQ ID NO 133
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (94)..(94)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(96)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (425)..(425)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 133

```
gcgacaaggt tgtgatccac gtggcaggtg ttcagaaggc tgggggcggg cagcgctggg         60

gagagccctg ggtacttcga ggagaccccg aagngnggct gctcccacac ctgcgccagt        120

ttccaccctc tctgtgagca gggctgcggt cacctccac atctgaagag aaccaacctg         180

aggatttcac gctggctgcg tgccagacca gtccctgaca ggttgtgcga ggcccttcgc        240

tggacagccc attgctggcc actgacgga gaggcagagg gggctgaaat tcgggcccat         300

gcctctgtga gcgatgacgg agcaacagct ctccagcacg tgaagctctc cagacagctg        360

ttcgtgagaa gccagacaga ggcctggggt ctcagtccag atttctgggg agtggggtgt        420

ccaancgtgg gccacgctgc tgggagccac ctagggaagc aggtcgcctg tttctatagt        480

gac                                                                     483
```

<210> SEQ ID NO 134
<211> LENGTH: 496
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

```
gggaaaaccc ttgtacctga agcatgagcc actcagaact caccaaaata ttcgacacca         60
```

```
taacaacaga tgctcaaact gtaaaccagg acaacaagtg gatgacttca cactgtggac      120

agttttttccc aagatgtcag aacaagactc cccatcatga tgaggctctc ccccctctta      180

actgtccttg ctcatgcctg cctctttcac ttggcaggat aatgcagtca ttagaatttc      240

acatgtagta gcttctgaga gtaacaacag agtgtcagat atgtcatctc aacctcaaac      300

ttttacataa catctcaggg ggaaatgtgg ctctctccac cttgcataca gggctcccaa      360

tagaaatgaa cacagagata ttgcctgtgt gtttgcagag aagatggttt gtatgaagac      420

gtaggaaagc tgaaattata atagagtccc ctttaaatcc acattgtgtg gatggctctt      480

gccgtttcct aagaga                                                      496
```

```
<210> SEQ ID NO 135
<211> LENGTH: 479
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (305)..(305)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 135

gagtccgagg atttcagggg cagctgggcg caggagctgg tgggctgttg ggagtgcccc       60

tttactgggc aggcttcctt cctcctggtg atgggggggtt cctcagcaca aaagtgaagg      120

ggtggagggg ctggaggagc aggaatctct cttgttgata ggtatgaggc cttgaagtcc      180

ttttctttgt cccaggattc atggacgctt cggggctgat cttttgagttt tcaagcatgg      240

ggtgcagaga cgtttaggta aactcttacc gtcctctctc ttcgtcaggg cttcccagga      300

atcancaatg cccaagaagg aagggattgt agaaatagct taacccttc atttaccaac      360

gtggaaattg aagcccaggg aagggaaggg accggtcgtg gaagggagag ccatcagcag      420

aaagagaccc tgagatcttc gcctgggatt cccaggaagt ccagcccgag ctgattcac       479
```

```
<210> SEQ ID NO 136
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(101)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 136

tcccaagccc ttagggaccg cagaggactt ggggaccagc aagcaacccc cagggcacga       60

gaagagctct tgctgtctgc cctgcctcac cctgccccac nccaggcccg gtggcccca      120

gctgcatcaa gtggaggcgg aggaggaggc ggaggagggt ggcaccatgg gcccgggcgg      180

tgccctccat gcccgggggа tgaagacact gctgccatgg acagcccgtg ccagccgcag      240

cccctaagtc aggctctccc tcagttacca gggtcttcgt cagagccctt ggagcctgag      300

cctggccggg ccaggatggg agtggagagt tacctgccct gtccctgct ccctcctac       360

cactgtccag gagtgcctag tgaggcctcg gca                                  393
```

```
<210> SEQ ID NO 137
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137
```

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```
aacctatcgc tgacttagca accaaagcct ccatcgttag gcaaggaata aaataaaacc      60

agcacgcttt ttccactgtg attttaaaa gtcattaaaa aatatctttt cccttatgta      120

cagaaaaatt ggaacagaaa aatatctaac ttgctgagca tttgatggga aaaagtaaaa      180

gataacttcc atttggtaca caacttattg tacatagagc tatgatttga ggaggcatct      240

aatttctgaa caaattcacc aagaaatacc atcacttaaa gtcattatcg caatcatgct      300

gcagtgaaca ctctatacaa aatggccagg tcattaaaca tcaaagatgg aaaacaagcc      360

agcaatctct tctgttc                                                    377


<210> SEQ ID NO 138
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

tgggcctcac ctatgatggg atgctgagtg atgtccagag catgcccaag actggcattc      60

tcatacttat cctaagcata atcttcatag agggctactg cacccctgag gaggtcatct      120

gggaagcact gaatatgatg gggctgtatg atgggatgga gcacctcatt tatggggagc      180

ccaggaagct gctcacccaa gattgggtgc aggaaaacta cctggagtac cggcaggtgc      240

ctggcagtga tcctgcacgg tatgagtttc tgtggggtcc aagggctcat gctgaaatta      300

ggaagatgag tctcctgaaa tttttggcca aggtaaatgg gagtgatcca agatccttcc      360

cactgtggta tgaggaggct ttgaaagatg aggaagagag agcccaggac agaattgcca      420

ccacagatga tactactgcc atggccagtg caagttctag cgctacaggt agcttctcct      480

acc                                                                   483


<210> SEQ ID NO 139
<211> LENGTH: 200
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

ttttgcttgt cttattggcc cagcaaccag cttgacactg gggactatca ggctccaaat      60

aataaccaat gtctcactcc aaacagacag gatactacgg agccagggtc agcaaacatt      120

ttctgtaaag ggccagatag taaatatttt gggctttgtg ggccctatgg tctctgtcac      180

aacgattcaa ctctgctgtt                                                 200


<210> SEQ ID NO 140
<211> LENGTH: 243
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

gagcgcctcc agtctagaag gcataagcca ataggataat atattcaggg tgcagggtgg      60

gtaggttgct ctggggatgg gtttatttaa gggagattgc aaggaagcta tttaacatgg      120

tgctgagcta gccaggactg atggagcccc tgggggtgtg ggatggagga gggtctgcag      180

ccagttcatt cccagggccc catcttgatg ggccaagggc taaacatgca tgtgtcagtg      240

gct                                                                   243


<210> SEQ ID NO 141
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

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```
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (185)..(185)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (187)..(187)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (189)..(189)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (199)..(199)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (204)..(204)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (206)..(206)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (211)..(211)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (219)..(219)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (223)..(223)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (237)..(237)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (246)..(246)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (265)..(265)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (269)..(269)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (275)..(275)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (278)..(279)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (407)..(407)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 141

tgagtgggct ttgagagagg gggaagagtg agtctgagca cgagttgcag ccagggccag        60

tgnggagggg gtttgggcca gtgcaccttc cggggcccca tcccttagtt tccactgcct       120
```

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```
cctgtgacgt gaggcccatt cttcactctt tgaagcgagc agtcagcatt cttagtagtg          180

ggttncngnt ctgtnggang actntngaga ntattcttng ttncctgttg gagttgntca          240

aatgtncctt ttaacggatg gttgnatgng cgtcngcnnc caggtttatg aatgacagta          300

gtcacacata gtgctgttta tatagtttag gagtaagagt cttgtttttt attcagattg          360

ggaaatccat tccattttgt gaattgtgac ataataatag cagtggnaaa agtatttgct          420

taaaattgtg agcgaattag caataacata catgagataa ctcaagaaat caaaagatag          480

ttgattcttg ccttgtacct caatctattc tgtaaaatta aacaaatatg caaaccagga          540

tttccttgac ttct                                                            554
```


```
<210> SEQ ID NO 142
<211> LENGTH: 479
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

ggacatggtt atctacagca ctgagataca ctactcttct aagggcacgc catctaagtt           60

tgtgatccca gtgtcatgtg ctgcccccca aaagtcccca tggctcacca agccctgctc          120

catgagagta gccagcaaga gcagggccac agcccagaag gatgagaaat gctacgaggt          180

gttcagcttg tcacagtcca gtcaaaggcc caactgcgat tgtccacctt gtgtcttcag          240

tgaagaagag catcccagg tcccttgtca ccaagcaggg gctcaggagg ctcaacctct           300

gcagccatct cactttcttg atatttctga ggattggtct cttcacacag atgatatgat          360

tgggtccatg tgatcctcag gtttgggggtc tcctgaagat gctatttcta gaattagtat         420

atagtgtaca aatgtctgac aaataagtgc tcttgtgacc ctcatgtgag cactttttga          479
```


```
<210> SEQ ID NO 143
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

cagttgctgc cctacatgga gaacaggagg ggtgctgtca tcctggtctc ttccattgca           60

gcttataatc cagtagtggc gctgggtgtc tacaatgtca gcaagacagc gctgctgggt          120

ctcactagaa cactggcatt ggagctggcc cccaaggaca tccgggtaaa ctgcgtggtt          180

ccaggaatta taaaaactga cttcagcaaa gtgtttcatg ggaatgagtc tctctggaag          240

aacttcaagg aacatcatca gctgcagagg attggggagt cagaggactg tgcaggaatc          300

gtgtccttcc tgtgctctcc agatgccagc tacgtcaacg gggagaacat tgcggtggca          360

ggctactcca ctcggctctg agaggagtgg gggcggctgc gtagctgtgg tcccagccca          420

ggagcctgag ggggtgtcta ggtgatcatt tggatctgga gcagagtctg ccattctgcc          480

agactagcaa tttggggggct tactcatgct aggc                                     514
```


```
<210> SEQ ID NO 144
<211> LENGTH: 265
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(75)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (79)..(79)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (126)..(126)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 144

gtgtggtgtt tgtgtcttaa ctatgcactg ggcccttgtc tgcgtcggct tgcatacaga        60

gggcccctgg ggtnngccnt ccggcctggc ctcagccagt gggatggaca gggccaggca       120

ggcctntgaa cttccacctc ctggggcctc ccagacctcc tgtgccccca cctgtgtggg       180

caggtgggcc agtcttcggg tgatgggacc aaaccccttc agttcagtag agaaaggcta       240

ggtcctctac aaagagctgc aagac                                            265


<210> SEQ ID NO 145
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(57)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (114)..(115)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (130)..(130)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (144)..(144)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (177)..(177)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (189)..(190)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (192)..(192)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (218)..(218)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
```

```
<221> NAME/KEY: misc_feature
<222> LOCATION: (225)..(225)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 145

ggaggcgcag aagattgatc gcatgatgga ggctttcgct tctcgctact gcntgtncaa       60

ncccggggtc ttncagtnca cnaggtcagt gcagagccca cagcctggcc cctnnccagg      120

cacagcctcn agctctggag gggncggccc ctgtgggcac agccnagcgt gtgttcntgg      180

ggacctgcnn tnccctgagc gaggacgacc tgtgggcngg gcacntcttg caggcgggcc      240

cccagcacgc ggggtcccac tgtccactgg aggttctggc tgagcccagc accccggact      300

cgttgcagac acgtgctacg tgctgtcatt cgccatcatc atgctcaaca ccagcctcca      360

caaccacaac gtgcgtgaca agcccacggc agaacggttc atcgccatga accgcggca       419


<210> SEQ ID NO 146
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (411)..(411)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 146

tatgagaaac ctctgcgacc attcccagat gatgtctgcg ttgtccctga gaaatttgaa       60

ggagacatca agcaggaagg ggtcggtgca tttcgagagg ggccgcccta ccagcgccgg      120

ggtgccctgc agctgtggca atttctggtg gccttgctgg atgacccaac aaatgcccat      180

ttcattgcct ggacgggccg gggaatggag ttcaagctca ttgagcctga ggaggtcgcc      240

aggctctggg gcatccagaa gaaccggcca gccatgaatt acgacaagct gagccgctcg      300

ctccgatact attatgagaa aggcatcatg cagaaggtgg ctggtgagcg ttacgtgtac      360

aagtttgtgt gtgagcccga ggccctcttc tctttggcct tcccgacaa ntcagcgtcc      420

agctctcaag gctgagtttg accggcctgt cagtgaggag gacacagtcc ctttgtccca      480

cttggatgag ag                                                          492


<210> SEQ ID NO 147
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 147

aatattgtct cataagcatc tttctatatt tgttcacatc gtacataatc atgttttttgc      60

acagatacat taatattatc atagtttgtt taactacttg gctttttcta acagtttttt      120

tttttgagat ggtcttgctc tgttgcccag gctggagtgc agtgacgtga tctcggctca      180

ctgcagcctt gacttcctgg gctcaagtga tcatcccacc tcagcctcct gagtagctgg      240

gactacaggt atgcaccacg accagctaat ttttttgtatt tttttttttgt agagagggta     300

ttttgccatg ttgcccaggc tagtcttgaa ctcctgggct caagcgatct gcctgcttca      360

gcctcccaga gtgctaggat tacaggcatg agccactgca cccagcctct taacaaattt      420

tgaatataac tcctgtctta aaatctgcag aatattgaat ttttccagct attttttact      480

tttgcttagc ttatagatgc taaaggatac tgtcatttgc atttttta               527


<210> SEQ ID NO 148
<211> LENGTH: 476
```

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (105)..(105)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 148

ctctctcact ttctatagct ttgttggacc agatggtgag gaaaggaatn ggcctcttcc      60

cttctagagg gggctggctg gagtgagacc tnggggcttg gcctnggaac ccaccacaca     120

gccccaaagt caggaagcct ggggaaacca gagctgagac ctcttcaaca gggtttcttt     180

gagatcctac acctccattg ggcccttttt cagtcttcaa tgggggccca gttggctcta     240

gaaggagaag aggtgaagca ggatcctttg ccctggggga gtctgagggc gcggtccttg     300

gactcattca ggccgtcttt gtagttgggg gagttccact gggcgatccc agccctccc      360

cacccaccct ctaatggacc tcctcataga agccccattt cacttttgtt ttatctacct     420

cttagcaaaa caatagataa attaggtagt ggcagctcca cttgcttagg ttaggg         476


<210> SEQ ID NO 149
<211> LENGTH: 177
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 149

gggagtttga ccagagatgc aaggggtgaa ggagcgcttc ctaccgttag ggaactctgg      60

ggacagagcg ccccggccgc ctgatggccg aggcagggtg cgacccagga cccaggacgg     120

cgtcgggaac cataccatgg cccggatccc caagaccta aagttcgtcg tcgtcat         177


<210> SEQ ID NO 150
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (109)..(109)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (146)..(147)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 150

ctaaccactg aggctctcta atcttcctct ggagttttag tgaaaggatt tattgagcag      60

cttctggaat ataatgtgca tgtccaaaat gaactcagcg cttcaaaang acnaagtctg     120

tagcctggag gggcttgagt ggatgnnagc tgatgctgtg attttgagct gtggttacat     180

gcagtcagta aacctgtgag actgctggag gaaatgtagc agacagcatg gaggctggga     240

cccagcagct actttgggtc atgtctttac tgtcctgcct ccaacccttt agtctcgtag     300

acttttgttc ttgtggaaat ttcttctgta ttccagttgt gtaaatatgt atggaaaact     360
```

```
gatattacta ggttttacgt tgcatctcca gtattgatct ttggaaactg atgttacatt      420

aggttccaat tcgcaatagt agcagagact gacatgcttt tattgagctg ctaagccccg      480

tggatgatgg agcgaga                                                      497
```

```
<210> SEQ ID NO 151
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (393)..(393)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (403)..(403)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (417)..(417)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (431)..(433)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (435)..(435)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (440)..(440)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (442)..(443)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 151

gccgacagct cctttaattt catggcgttt ttcttcatct tcggagccca gtttgtcctg       60

accgtcatcc aggcgattgg cttctccggc tggggcgcgt gcggctggct gtcggcaatt      120

ggattcttcc agtacagccc gggcgctgcc gtggtcatgc tgcttccagc catcatgttc      180

tccgtgtcgg ctgcnatgat ggccatcgcg atcatgaagg tgcacaggat ctaccgaggg      240

gctggcggaa gcttccagaa ggcacagacg gagtggaaca cgggcacttg gcggaaccca      300

ccgtcgaggg aggcccagta caacaacttc tcaggcaaca gcctgcccga gtaccccact      360

gtgcccagct acccgggcag tggccagtgg ccnttagagg gangcctgcc ctgcccncac      420

cgccaccac nnncnccccn tnnttcctgc tgctacccct gtgtcccgag ggctgggagt      480

acctggggcc ccatcccccc agctgtgatg gtggaagccg gtggtggcc                 529
```

```
<210> SEQ ID NO 152
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (145)..(146)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 152

agatgaagcc cttcaagcgc tacgtgaaga agaaagccaa gcccaagaaa tgtgcccggc       60

gtttcaccga ctactgtgac ctgaacaaag acaaggtcat ttcactgcct gagctgaagg      120
```

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```
gctgcctggg tgttagcaaa gaagnngacg cctcgtctaa ggagcagaaa acccaagggc    180

aggtggagag tccagggagg caggatggat caccagacac ctaaccttca gcgttgccca    240

tggccctgcc acatcccgtg taacataagt ggtgcccacc atgtttgcac ttttaataac    300

tcttacttgc gtgttttgtt tttggtttca ttttaaaaca ccaatatcta ataccacagt    360

gggaaaagga aagggaagaa agactttatt ctctctctta ttgtaagttt ttggatctgc    420

tactgacaac ttttaga                                                    437
```

```
<210> SEQ ID NO 153
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 153

ttctttcaca ccctgtcggg agaatgtgtg ccctgcgact gtaatggcaa ttccaacgag    60

tgtttggacg gctcaggata ctgtgtg                                         87
```

```
<210> SEQ ID NO 154
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 154

cccgctggtg cagtggaaga gcccggcggc cgccgccgca gccttctcgg cccgcgcccc    60

cgccgcctgc acccccatct gctcttcccc gcggggggccg cgcggcgcgg gctggggggcc    120

cgggcagccg cgctcgggca gcgggggcgc ggggctgccg cctgcgctcg cagctggtgc    180

cggtgcgcgc gctcggcctg ggccaccgct ccgacgagct ggtgcgtttc cgcttctgca    240

gcggctcctg ccgccgcgcg cgctctccac acgacctcag cctggccagc ctactgggcg    300

ccggggccct gcgaccgccc ccgggctccc ggcccgtcag ccagccctgc tgccgaccca    360

cgcgctacga agcggtctcc ttcatggacg tcaacagcac ctggagaacc gtggacc      417
```

```
<210> SEQ ID NO 155
<211> LENGTH: 407
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 155

taagagactg agccgctagc agcgcctggg gaccagacag acgcatgtgg caaagctcac    60

catcttcact acaaacacgc ctgagagtgg cactggggaa acataactcc atctacacct    120

tggatttgga ctgattctcc attttatcac ctgaaggctt gggccagagc tcaacagcta    180

ctcaactgga ggggtgaggg ggataaggtc tgtagtatac agacaggaag atggtaggtt    240

tatgccttct gtggccagag tcttggactc atggaaatag aatgaataga ggggcattca    300

caaggcacac cagtgcaagc agatgacaaa aaggtgcaga aggcaatctt aaaacagaaa    360

ggtgcaggag gtaccttaac tcacccctca gcaaatacct atgtcaa                  407
```

```
<210> SEQ ID NO 156
<211> LENGTH: 399
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

gagaccagtt cacggggcaa gagatgaacg tggcccagtt cctcatgcac atgggcttcg    60
```

```
acatgcagac ggtggcccag ccgcagggac tggagcccag tgagctgctg gggatgctga      120

gcaacggaag ctaggcagac tgtctggagg aggagccggc actgaggggc ccagacaccc      180

gctgccccag tgccacctca cccccacca gcaggccctc ccgtctcttc gggacagggc       240

cccagccgtc cccctgtct gggtctgccc actgccctcc tgccccggct ttccctgccc        300

ctctcccaca gcccagccag agacaaggga cctgctgtca tccccatctg tggcctgggg      360

gtccttcctg acaacgaggg ggtagccaga agagaagca                             399


<210> SEQ ID NO 157
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

gtgaccagta ccgcaagggg atcatctcgg gctccgtctg ccaggacctg tgtgagctgc       60

atatggtgga gtggaggacc tgcctctcgg tggccccggg ccagcaggtg tacagcgggc      120

tctggcggga caaggatgta accatcaagt gtggcattga ggagaccctc gactccaagg      180

cccggtcgga tgcggccccc cggcgggagc tggtactgtt tgacaagccc acccggggca      240

cctccatcaa ggaattccgg gagatgaccc tcggcttcct caaggcgaac ctgggagacc      300

tgccttccct gccggcgctg gttggccagg tcctgctcat ggctgacttc aacaaggaca      360

accgggtgtc cctggcggaa gccaagtccg tgtgggccct gctgcagcgt aacgagttcc      420

tg                                                                     422


<210> SEQ ID NO 158
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (364)..(364)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (373)..(373)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (375)..(376)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (378)..(380)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (383)..(384)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 158

acgcagcccg cgacaacaaa aagacccgca tcatcccgcg ccacttgcag ctggccatcc       60

gcaacgacga ggagctcaac aagctgcttg gtaaagttac catcgctcag ggcggtgttc      120

tgcctaacat ccaggccgta ctgctcccca agaagactga gagccaccac aaagctaagg      180

gcaagtaagg gctgaacttt aaaaatgtaa acttacaaga caaaaggctc ttttcagagc      240

cacccaccat ttctacggaa gaactgagca ctctgttctc caaacctatc agaaatttgt      300

ggccgagttc aagcactgag gccattactt tcctattggg taaaataaaa gtattgaatc      360

aggnctagta aanannannn aanngctacc ttataacatg aaggaacctc ctta            414
```

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<210> SEQ ID NO 159
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 159

tatcaagatt gcccctgcgg aaggcccaga cgtcagcgaa aggatggtca tcatcaccgg        60

gccaccggaa gcccagttca aggcccaggg acggatcttt gggaaactga aagaggaaaa       120

cttctttaac cccaaagaag aagtgaagct ggaagcgcat atcagagtgc cctcttccac       180

agctggccgg gtgattggca aaggtggcaa gaccgtgaac gaactgcaga acttaaccag       240

tgcagaagtc atcgtgcctc gtgaccaaac gccagatgaa aatgaggaag tgatcgtcag       300

aattatcggg cacttctttg ctagccagac tgcacagcgc aagatcaggg aaattgtaca       360

acaggtgaag cagcaggagc agaaataccc tcagggagtc gcctcacagc gcagcaagtg       420

aggctcccac aggcaccagc aaaacaacgg atgaatgtag cccttccaac                  470


<210> SEQ ID NO 160
<211> LENGTH: 383
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

agagagactc agagacccgg gagggccttc ctctgaaagg ccaagccaag ccatgcttgg        60

cagggtgagg ggccagttga gttctgggag ctgggcacta ctctgccagt ccagagttgt       120

acagcagaag cctctctcct agactgaaaa tgaatgtgaa actaggaaat aaaatgtgcc       180

cctcccagtc tgggaggagg atgttgcaga gccctctccc atagtttatt atgttgcatc       240

gtttattatt attattgata atattattat tactattttt ttgtgtcatg tgagtcctct       300

ctccttttct ctttctgaca ttccaaaacc aggccccttc ctacctctgg ggctgcttga       360

gtctagaacc cttcgtatgt gtg                                               383


<210> SEQ ID NO 161
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

aggatgcccc tttgagaaat gctgttccac agaaccctgc ctttcaggcc ttggagacgt        60

gggcagggga gaagcagcgt ccctcagagc caggcctggc agtggtgcta gcaggggcca       120

aggccaggga gcagggtctc ctgtcggagg gacctgggca agcccctcca cgcgccagcg       180

ggtttctcag caggggaggt ccacaccaca ccgcttggga acctgggtgc ctaaacgcaa       240

caggagccaa ggcacaaatt taaccaaaca ccaaggttgc gtgaggcccc atttcatgag       300

ccgggctcca aggacgtgtc cttaggcggc tctggaaggc ccagcgccag cccccgtcct       360

ctgttaaagg gagccagccc cggcgtccgc ccaggcatgg tagcctgagc gcgccccag       420

ggtagtaggg ggcacctgag gagcagggtc tgccctggca tgagcagagc ccag             474


<210> SEQ ID NO 162
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (134)..(134)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

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```
<400> SEQUENCE: 162

gatacttgga tgcttttcct ctgactgatg aagatcctga ataccaaaga gggccgctga     60

caggtctagg agtacacttc tagcacctag cagagagagg cttcactaca tcatgcttcc    120

tgacatctct cccnttgaag agcagtcaga ctcctgcttt gctcttcaga cttaatttgg    180

gggtttaaca ggtgaggttg ctgggggaac tcttttacaa catctctctg aaagaatccg    240

ggctgccagt ttcatttggt ttgggtgtca gtagcatgat ggaaagacaa aaaaacacaa    300

cttgacatct gcagaaatgg gttcaaattt tacctgcaac tcaccaattc tgtggccttg    360

gttcagcaat t                                                         371


<210> SEQ ID NO 163
<211> LENGTH: 445
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

caacaagacg gacctggctg ataagaggca gataaccatc gaggaggggg agcagcgcgc     60

caaagaactg agcgtcatgt tcattgagac cagtgcgaag actggctaca acgtgaagca    120

gcttttтcga cgtgtggcgt cggctctacc cggaatggag aatgtccagg agaaaagcaa    180

agaagggatg attgacatca agctggacaa accccaggag cccccggcca gcgagggcgg    240

ctgctcctgc taatgcagag ccgacctgtg gcttcccatg acactccttg cttgttgtgt    300

tgcttcctat tggctagctt cctaaggggg gagggaaccg agttatcaag atgggaggat    360

ttttcttttc tctctgtctt taggagtagg gtgggatggg gagggaggct gggcatcagg    420

gatcacatca ctcttaacgg ctgtt                                          445


<210> SEQ ID NO 164
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 164

ggtggcctct ggatcctccg tggaccgaac cgtcccccca ggaacacacc ttcaggtaga     60

ccccgaagcc tcaaggccgg ggctggagcg gagaccccag ggcctctcag gagacagtga    120

ggctgcccct cctaccacct acctcattct gcctactcac cccagggggcc acagccacag    180

cctgctggac tcaggactgt cctgtcaact ccagacaact gaataaacag gccgggtaca    240

gtggctcgca cctgtaatcc tagcactttg ggaggccgaa gcgggtggac cacttgacgt    300

ccgtagttcg aga                                                       313


<210> SEQ ID NO 165
<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

aatgtcatgt ttattcaggc tgggaactgt attcacagta gaagtttcag tggtcaacat     60

atctatgact ctttaggctg ctgtagtttt acagtcaatt atttaaaagt gagtagttac    120

atttataaga gcctgagaat acttagactc agtcatttgt tagtattttt accaaaatct    180

cttagtttca gacatgtcag aagcagctat atagcatatc ttattctatg atatacatca    240

ggctatctca agttcctgtc tcacagttaa ttcaaagaag gattaggatt tctgtatttt    300

ttctcatttg aatctttatg tgcatttggt ttgtgtacat gctt                     344
```

<210> SEQ ID NO 166
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

```
tcttaccccca ctgaaaccaa cagggatcgg gccaggctcc cagattcttg aggacaggga      60

cttcggcatt tactaatggg ggactactgt ggggtaaggg ggcgcctgct tgcctgatac     120

aggatggggt caagggacag tgggcaggtc ctcactcagg agtggggggt gtaggctggc     180

cagcccccag ggcttgtcca ccagtcttct ccccgcaagg ccctcagagc agcgcctgtg     240

ggtgtcagta ttacctgagc ctaggccaaa gctagcccaa ggctggggaa ggggaggaga     300

ctccaggtca gaatgtgagg tctcagtctg tgatttaagg tgttgcatgt ggactcttaa     360

ctgtacgtgt agtttctagt ggagaaatca aggctctgat cattttgttt ttagtatgaa     420

aatgtgattt cctttctgtt tgtaactc                                        448
```

<210> SEQ ID NO 167
<211> LENGTH: 334
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

```
agatgccagt aatcaatatt gaggacctga cagaaaagga caaattgaag atggaagttg      60

accagctcaa gaaagaagtg acactggaaa gaatgctagt ttccaaatgt tgtgaagaag     120

taagagatta cgttgaagaa cgatctggcg aggatccact ggtaaagggc atcccagagg     180

acaaaaatcc cttcaaggag ctcaaaggag gctgtgtgat ttcataatac aaacaaaaag     240

aaaaaaaatt aaacaaattc ttggaaatat ctcaaatgtt aataacaata tgaattttc     300

tcatgcatac tattactact aagcatgtac gtga                                 334
```

<210> SEQ ID NO 168
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

```
gcccccgact gaggcggaga cgaaggtgct gcaggcgcga cgggagcggc aagatcgcat      60

ctcccggctc atgggcgact atctgctgcg cggttaccgc atgctgggcg agacgtgtgc     120

ggactgcggg acgatcctcc tccaagacaa acagcggaaa atctactgcg tggcttgtca     180

ggaactcgac tcagacgtgg ataaagataa tcccgctctg aatgcccagg ctgccctctc     240

ccaagctcgg gagcaccagc tggcctcagc ctcagagctc ccctgggct ctcgacctgc      300

gccccagccc ccagtacctc gtccggagca ctgtgaggga gctgcagcag gactcaaggc     360

agcccagggg ccacctgctc ctgctgtgcc tccaaataca gatgtcatgg cctgcacaca     420

gacagccctc ttgcagaagc tgacctgggc ctctgctgaa ctgggctcca gcacctccct     480

ggagactagc atccagctgt gtggccttat ccgcgcatgt gcggaggccc tgcgcagcct     540

gcagcagcta cagcactaag a                                               561
```

<210> SEQ ID NO 169
<211> LENGTH: 244
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

```
<221> NAME/KEY: misc_feature
<222> LOCATION: (94)..(94)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (128)..(128)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 169

aatgtgtatg tctgggtaag tgtatagatt ttacaactat tttgaaggcg acctttttaa      60

ctttaaacag accactctgg aggagacgcc tganccagag cgctttacct aaagttcggt     120

gcctaaantg cacccttcct ctggctggtg tctcccttct gccaagctat gcctcctgca     180

gaggtaggct ccgtggtgtc tcccactccg ccccaactgg agaacggtgt aaagaactgt     240

cagc                                                                  244


<210> SEQ ID NO 170
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (262)..(262)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (268)..(268)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 170

caggatggca ttagctctgt gtctgcaggt gctgtgcagc ctgtgtggct ggctctcgct      60

ctatatttct ttctgccacc tgaataagca ccgaagctat gagtggagct gccgcctggt     120

caccttcacc catggagtcc tctctatagg cctctccgct tatattggct tcattgatgg     180

cccatggcct tttacccacc caggctcacc caatacacct ctccaagttc atgtcctgtg     240

tctcaccttg ggctacttca tnttcganct tgggctgcat ctggcgcttt gcatggagga     300

agagcatcaa gaagtaccat gcttggagaa gcaggcggag tgaggaacgg cagctgaaac     360

acaacggaca tctcaaaata cactagccaa ggcttgctcc agattatg                 408


<210> SEQ ID NO 171
<211> LENGTH: 359
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

aggacatcga ggctgcggtg aaccatgatt gtaccactgt attccagcct ggacgactga      60

gtgagaccct gtctcaaaca aaacaaaaca aaacaaaaaa aagtacaaga ggaaaaaaat     120

tgatttctga ttgcctcact caagataagg tcaacattga aggtggaggt ggaagatgca     180

gtttatgtag gggtctgaag attttaccat tctggggact gtcttaaga aagagaatcc      240

aaaattaggt agaaaagtga acgtctgacc gggcgcggtg gctcatccct gtaatcccag     300

cacttaagga gtacgagacg ggaggatcac gaggtcaaga gatcgacagc atgctggcc     359


<210> SEQ ID NO 172
<211> LENGTH: 386
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (182)..(182)
<223> OTHER INFORMATION: n is a, c, g, t or u
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<400> SEQUENCE: 172

gtttctgcct ttgaacgtgg ctgtgggaag acatgatgct tagtgttgct gcagctatct   60

catgaccttg ggcaaaacat cccaacacac aggagggcca aacaagcagt cagaagaagc   120

ctgagtcttg tgggtgttgt tgagcagctg aacaaaccct aggatggctt ccttccagac   180

tncttaggat tgcgaacaat gaagctctat tgtttaagca aggtatcgat ggctattttc   240

acttgccact gaaagcacca ggacagagaa tcgtctttct aggaatacag ccacaaaagc   300

cttcattatg gtatatgcac ataaagaata taaaagtttc ctttatgttt ctctttaaaa   360

tatagctgaa gtctgcctca ggcaaa   386

<210> SEQ ID NO 173
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

ggttccaggc tttgcatctg gagcctttac cggttgactg ttgccttcca cacaaacagc   60

ctctgaaaag cactttctcc atacataatt ctggagaaga tgagggatct tgccctccag   120

gagccttcct tcctccccca atgaggaaat cagtcactgc actggtgcaa aggcaagcag   180

attggaattt ctgctcttca ccgattttct cagggaaaga ccccttcccc ttgccagcag   240

aggaacctgt agttttttcc atttctttct tcagaaccaa agtatgtatc actcctcatg   300

ctcacaggga ttgacaggag agaattcacc aggatcttag ctcaaaagac acagcctcag   360

aatggccaga tggattgcac gaaacctgac ttggattcac catcttcc   408

<210> SEQ ID NO 174
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (227)..(227)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 174

gtggacgagt gactgtccct ggtttgggct ggtgccattt agagggcaac cagagtgcag   60

ggaagggagg agcttgggca agagggacat tgctgtcgct ggttgatggt gagatggcac   120

ttaatgagaa cctggtcatt gggaaagccc caagcctgcg tcttgctgtg atgccttccc   180

cattatgaag ggtccattgg catgggagtg gggagacctg gactcanana agctacaagg   240

gcaagggtgg aaaggcatag cttntgcaag ttgatgctga aaaagatcca agactcatat   300

tcagcagaca gcccataacc aagagccaag g   331

<210> SEQ ID NO 175
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

aggtcttcaa agaattggcc agtcttacag ctcaccttgg ggtgtagatg actctccact   60

gtggtgctag gcaattttat tgaacaggtg gccactggtg gtgatggctg aaccactcat   120

taaacaaatt gctctaaatg gcctcagtat caaggtgtgc tttctgtacc cttaatctga   180

ctttaatcct gcagaacctc agtcttacca tgtttaacag cattgccatg tacgatatgc   240

ctttatccta cactgtatat   260

<210> SEQ ID NO 176
<211> LENGTH: 528
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

gctggctatg tacatggtcc cattccctac ctgcacttct ttatgcctgt cttcaccctg   60

ctgaccatcc acagcagcca gcactaccag gccctcatag tgcctgagct cacccagcag   120

atggttgatg ccaagaacat gatggttccc tgagacccct gccatggcca ctacctaaag   180

gtggccacag tgttcacgga ctacatgtcc atgaaggagt tggatgagca aatgcttaat   240

gtccaaaaca agaacagcag ctactttgtt gagtgaatcc ccaactatgt gaaaacagct   300

gtctgtgaca tcccactctt ggggctataa atgtctgcca ccttcaacat caacagcgtg   360

gccatccagg agctgttcaa gcacatctct gagtggtcat gtttcggtgc aaagcctttc   420

tgcactggca catgggcaag agcatggact agatggagtt caccaaggct gagagcaaca   480

tgaacaacct ggtgtcccgg taccagtaat accaggacac ctcagcca   528

<210> SEQ ID NO 177
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (31)..(31)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (48)..(49)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (52)..(52)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (64)..(64)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (76)..(76)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 177

acttatctgt gctgtaacta ttgaaatgaa nccncttcaa atatgtannc cncntttctt      60

tttnanattt ctaganangg tttcaatata gactttctga cttttatggt atacatatag     120

gncaatattc tattcttctt tcctttttaaa tacttactgt ttcaatttca aataaaaaat    180

cagcattcta gtttgtacat tttagcacag aaatgtttac aaccttcagc acaattgctt     240

ttgtaattta ctgacttggc attttgaggc gtttttaaca aattatgaga aataacacct     300

tcagaaagca tgtgactact ttgatgcaac tatttacaat gtattcataa gaagtcatta     360

acctgtagag ttcttagaca tgtggaacct ttaacaatta tactaaagag tacatacaaa     420

atacagagct atgtaataat aactaatttt aaatcctgac aaattagaag ttaagcctac     480

tatctgtaaa aatatgtcct gattcatttt tttaagtata tacctgagcc tttaaaaagt     540


<210> SEQ ID NO 178
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (460)..(460)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (462)..(466)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (468)..(469)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(472)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (475)..(481)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (483)..(487)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (489)..(493)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (496)..(503)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (505)..(510)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (512)..(535)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 178

gccattttga gtgccagatc tagttatttt gctgcaatgc tgagtggctg ttgggctgaa      60

agctcccaag agtacgttac tcttcaaggt ataagccatg tagaactgaa tgttatgatg     120

catttttatat atggaggaac tctggacatt ccagacaaaa ctaatgttgg tcagatactc    180

aatatggctg atatgtatgg actagaagga ttaaaagaag tagcaatcta tattttaaga     240
```

-continued

```
agagattact gtaatttctt tcagaagcct gttcccagaa cattgacgtc tatactagaa        300

tgcctgatta ttgctcattc agttggagtg gaaagtcttt ttgctgactg catgaagtgg        360

attgtaaagc attttgcaag gtttttggtct gagagaagct ttgcaaatat acctcctgag       420

attcagaaaa gttgtcttaa tatgttgatt cagtccttan tnnnnntnnc nngannnnnn        480

ntnnnnntnn nnccnnnnn nnngnnnnnn cnnnnnnnnn nnnnnnnnnn nnnnncaggg          540

tgcactcaca gcacagaaca                                                     560
```

```
<210> SEQ ID NO 179
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

gggttcacgt cattttcctg tctcagcctc cccagtagct gggactccag gcacccacca        60

ccactcccgg ctaattttt gtatttttag tacagacagg gtttcactgt gttggccagg         120

atggtcttga tctcctgacc ttgtgatcca cccacctcgg cctcccaaag tgctgggatt        180

gcaggcatga atgaccgcgc ccagccgcag gcgcaacttt tttgagtttt cctggccagg        240

cgcggtggct caggcctgta gtcccagcat tttgggaggc cgaggtgggc ggatcacttg        300

aggtcaggag ttagaaacca gcctggccaa cgtggtgaaa ccccgtctcc agtaaacata        360

caaagccatt acagggcatg gtggg                                              385
```

```
<210> SEQ ID NO 180
<211> LENGTH: 173
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

gacaacctta gttcacttgg gtattcccat aatccttgtc tttcagggtt gacctgttac        60

agctgcttaa acacatcact gtatgctagg tattgcctac cttcacttac ttttctaacc        120

ttgccgatgt gctgccttca taaactgggt atatctccgc cacacttcta cgt              173
```

```
<210> SEQ ID NO 181
<211> LENGTH: 340
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (167)..(167)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 181

ggtaactttg gccaagactt ttcagtagga aatgcttcaa aatacaaagc aagagctatt        60

ttcaagaaag accttctaaa tttatattag gacatagtga gaagaaagcc atctgaaaac        120

caggaagaga gccctcacca gaatctgacc atgctggtgc cctgatnctt ggactttcag        180

cctccagaac tgcaaaattc tggtgtggtg tgaatgctgt ggctcagtcc gaacatgttt        240

ttttctgtaa ttttatcatt attacacgat tgcaatatca gttttgtttt ttaattggaa        300

agcaacattt tctactgttg aaagacgttt tttgacaaat                              340
```

```
<210> SEQ ID NO 182
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182
```

```
acagcttgtc tgtcacagtg cctgttctga ttgcaggctt tggtgttctc ctggtgttaa        60

tcctgacttt tttcctagtg atccaccctc tgggaaactt ctggctaatt cttagcgtca       120

cctcaattga gctgggcgtt ctgggcttaa tgacattatg gaacgtcgac atggattgca       180

tttctatctt gtgccttatc tacaccttga atttcgccat tgaccactgt gcaccactgc       240

ttttcacatt tgtattagca actgagcaca cccgaacaca atgtataaaa agctccttgc       300

aagaccatgg gacagccatt ttgcaaaatg ttacttcttt tcttattggg ttagtccccc       360

ttctatttgt gccttcgaac ctgaccttca cactgttcaa atgcttgctg ctcact          416
```

```
<210> SEQ ID NO 183
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (247)..(247)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (371)..(371)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 183

aggccgggct cagaggcgga gaagcctgcc tggtgcccac agccgtctgg ctcagggact        60

ccaccctggc cccgagtngc cgtntgctgg gcctttcctt cctggctctg cacccccatgc      120

tggctgcccg gtctggcttc ccttcttgtc tctgtcttgg gcgaggcagc tgtgagcatt       180

gcacagaggc aaagaccctc ctgcagcctn tgcgctgggc cgtagaaaca agagcctttg       240

taatacngaa cctcattcaa ggattaggag tggtggttag gtcagggcca cccccagtgc       300

tgcaggaacg gcctccaccc agctctgttg gtcagagcct gggtcatgca cctggagttg       360

ggagatcaag ntgggtctca gggcagtgag gtggccatat ccaccacatc gcatttcgtg       420

ggggaagagg tgacctcttt gttttaaact taaggtgtct gcttatccag ccagaaataa       480

aaatctgcca gtggtgttcc caa                                              503
```

```
<210> SEQ ID NO 184
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (294)..(294)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 184

gagtcccgtc tcagtgtgga ggaacnggct gcacatggga cctgaaggtg ccctctgtgt        60
```

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```
ttatgttggg ggtggggggg cagtgctggc tgcctctgtc ctgtgtgtga ccctaccctc        120

gaagggtcct gtcctgtcag tcccgaggga gccacaacca aagctgcgga gagaaggtgg        180

ggaagggtgc ggaatggccg tggggcacag cgtggcagac tgttcagtct ctgctgggtc        240

tttcctaggg acctggaagg ccagtgttgc ttccccctca ctccctttca ctgnaggcag        300

cctctctgct tccccaatgc cttatgcctg ggcacactgc cacagaatat gcaatatgtg        360

tgggtgacca tgccctc                                                       377
```

<210> SEQ ID NO 185
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

```
gtcatcctgt gctcagttag cagctcatcc agctgggtca ggaaagcctt ttggaagcgt         60

aggaccttgc cagccagcgc tgggatatgc aggaggacgg ggacagcatt cagcacctcg        120

cgcagaaagc ccgactcctc cttcagtccc tcctgagcta ggtccagcag cctgaggaag        180

cgagggtcgt cgtactcgaa gcggcgcccg caggtgaggg aggcgatcac gttgctcacg        240

gctttgtcca agagaccgtt ggggcgaaag gggcgtcgga gtggttggcg aaggcggcac        300

aaaggcaggc ggcctcctcg gtcacccact gctccagcga cttcttgccc aggcccaagt        360

tgcgcaaggt ggagacggag aagcgcctct                                         390
```

<210> SEQ ID NO 186
<211> LENGTH: 188
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

```
ggctggcaac ccagaaagat tggatttcag tgccatggtg ctggctgcgg agagcttcac         60

ctcagggagg cactactggg aggtggacgt ggaaaaggca accaggtggc aagtgggcat        120

ataccacggc tctgcagacg cgaagggcag cacggccaga gcttccggag agaaagtctt        180

gctcacgg                                                                 188
```

<210> SEQ ID NO 187
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (213)..(213)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 187

```
taggaatgga gcccgagcag tctcgctctc agggccctgt gtggagtcac tgtgctgtcc         60

cagctctgga gacgcagaat tccacatgag gaatgtggaa ttcagcatgg ggatgacgct        120

gcttcaccca gacttggagg agcgtggtga attgcccgtg cccatgctct gatgtgcctc        180

tctggccgct gcgttcctcc tttctccctg ccntgggtca gtgcctgtaa acactgccct        240

aaatcagcag ggcccccgtc acttctgctt tatgcacctt tttcctcaga cacattaata        300

cagggggagtt ttgtttccaa gggaccacat ccagatggag gggctgtttt tggtgatctg        360

cactgccaaa tgcccgagtg tccctgacag tcggagctga tgaggccaag gctgtgtgtg        420

gttcctctgg atggccagaa gaggaaccaa aacactgaat tctgggcctt cttaagagtg        480

gtgatcagca cattgtgata gaagcatatc tgggaatgaa cttggcctca agcttttggc        540
```

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```
cttttaatt                                                                549


<210> SEQ ID NO 188
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 188

ctactctctg tctccataaa ctggtctatt ttggacattt cacataagcc tccctggatc     60

ccagtttaag catcctgggg tttgtctgcc tgccagagcc atggtgccac tggggctacn    120

tgtcctgtgg gatgacaagg caggtccaaa cctttgcctg ctctcccatc cattcctttt    180

gtgttagtcc atgtgtctcc cgactgttct ctccaacaac aacacagact gacaaaacct    240

actgacttgg agtcaggaac agactttgct attttctggc tgtgtgatcc tgatgagtcc    300

cttgaacctc ctggacttgt tcctcagcct aaaaaccaag actaataaat caagtctatc    360

tcacagcctt acgtggggat caaaaaacat ggagcatgtg aacacacatt gtacatcacg    420

aagctgtgtg caaataaata tcgtgtaact ccagccctt                           459


<210> SEQ ID NO 189
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 189

gcccgaggcc tgctgagaag catgggggcc ttgggatagt tccagaatga ggatgtgcgt     60

ttctagctgc tttgcgccct cctcccccaa aaatctgcta ccacaattcc ancccggcgg    120

cacgccccca agactccttt gtcgccccag gggcgggacc tgagctgtcg gttttcaggag   180

cccttcgtga cttcaaaagt cctgggcact gttgctcatg agtgctgcac aactgtcgcc    240

ctctaaagcc acctccatcc ctcactgggc tggcctcctg agccttcggt gaggaaacgg    300

ggttccgagt tgcccgcctg agagcttaac agtctgacta gaaaagggct aattcgcttt    360

ctgtgcaaat ctcttgagct aattatttaa tctgaaacat ggacaggtaa aggaccattg    420

gcgggcgtgg                                                            430


<210> SEQ ID NO 190
<211> LENGTH: 406
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

acatcaagca gctttctcgc tttgctggag cttcaagtaa gattgctcca gtggaagcac     60

cagatgctaa ggtgaggatg gtgatgatcg ctggatcacc agaggctcgg ttcaaggctc    120

agggaagaat tatggaaaaa tgaaagaaga aaacttcgtt agtcctaaag aagaggtgaa    180

acttgaagct catatcagag tgccatcctt tgctgctggc agttactgga aaaggaggca    240

aaacggtgaa tgaacttcag aatttgtcaa gtgcagaagt tgttgtccct tgtgaccaga    300

cacctgatga gaatgaccaa gtggttgtca aaataactgg tcacttctat gcttgccagg    360
```

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```
ttgcccagag aaaaattcag gaaattctga ctcaggtaaa gcagca                    406


<210> SEQ ID NO 191
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

aatgctgtca gcccttaggc aagactaaat tggaaagaaa ggtgtctgcc aaagaaaaca     60

ggcaggcccc tgtcctcctt caaacataca gggaatcctg gaatggagaa aacatagaat    120

cagtgaaaca aagccgtagt ccagtttctg tgttttcctg ggacaatgaa aagaatgaca    180

aggactcctg gagtcaactt ttcactgaag attctcaagg ccagcgggtc attgcccaca    240

acactagagc tccttttcaa gatgtaacca ataactggaa ttgggactta gggccgtttc    300

ctaacagtcc ttgggctcag tgccaggagg atgggccaac tcaaaatctg aagcctgatt    360

tgctctttac ccaggactct gaaggtaatc aagttatcag acaccaattc taaatgtttg    420

aagctttgtt tctaaaagta ccttgaaatg atagagatgt aggaaaatat agttgtgggt    480

ggagagagga gtgagtttgt ttaggtggga aggtggcatg ggatgaagtt gtcattactg    540

agcatcttct ctgtg                                                     555


<210> SEQ ID NO 192
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

gccctgctca gaggtcagag ggtctgggca gaggagggac cacattcccc tgccttgccc     60

ctgagcactt ctggagactg cgtcctgtcc tatctgctca ccatcaccct tcctgcccga    120

cggagctgct tctgctccct ggggcatatg gactgaccca cctcctgctg agaaccttcc    180

cctaggccct gtgcagaagg gctactgccc cttaggcctc agctggggga aaggcagttc    240

tggtgctgta gaggccctgg tgcagaaagt gggacgtctt ttttcctaag gtgtttaagc    300

acaggcttga taagtttggt tttaaaaaa taatctagga aatgaataat tctaaatcta    360

gtaatgagga aactgagcat ttcttttgcc ctccagggtg ccaagaccct acatatgaca    420

gaacccttgg cccttctcca tgcctgtggg atctgtttct ttaaagcact ttgtactgtt    480

attcaggagg ttgataatct ccttgaccca tgtctttcta ccctaatccc cacttccctg    540

cagaatcaat ctga                                                      554


<210> SEQ ID NO 193
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

acgcgtccaa catctcaaac ttgatctcca tctttggctc cggcttctcg gggctggtga     60

gccgacagcc ggactcctcg gagcagccgc cgccgctcaa cgggcagctg tgcgccaagc    120

aggcgctcgc cagcctcggc gcctggactc gagccattgt cgccttctag gaccccga     180

gggcacaggg acccggggcc ccgcggggct ggggccagac aaagactcgg caaagggcg     240

agaggaggga acgagcgggc gccgggccac tcgggctga gctgggggcg agcggggca      300

ggcggctgat gttttataa                                                 319
```

```
<210> SEQ ID NO 194
<211> LENGTH: 218
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

gaagactttc taaataatga taatcagagc tgtactctct ctggaggcaa acatcatggt      60

cctgttgaag ccctgaaaca aatgttattt aaccttcaag cagtacaaga acgttttaat     120

caaaataaga ccacagatcc aaaagaagag attaaacaag tttcagaaga tgatttctct     180

aaattacagt tgaaggaaag tatgattcct attactag                             218


<210> SEQ ID NO 195
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

ccccacccaa atacaagtcc cagtggaaag gaaaggtagt acctattctt ctccatgggg      60

ttcctaacac cctccattac tctttcagtc tccaagcact ttgaatccat tttttaaacat    120

tcaggttgcc agacctgtca cacagtgggc tctgataggg ttacggaggg ggcctggctc     180

tcagtctcta ctctcctatg tcccatcagt tggttggagg ccaccttcca gggggtatgg     240

gagaca                                                               246


<210> SEQ ID NO 196
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

caccttgacg gttccagtgt ctgtatttat gttgaaagtc caggtgaatg acatcatcag      60

tcgtcagtac ctgagccaag cagttgtaga agtgtttgta aactacacga agacaaattc     120

cacagtaact aaaagcaatg gagcagtgct gataaaagta ccctacaaat taggacttag     180

tttaactatt attgcttaca aagatggcta cgtgttgacc cctctgcctt ggaaaaccag     240

aagaatgcca atatattcat cagttacact ttcactgttc ccg                      283


<210> SEQ ID NO 197
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

cgtccgagtg tgagtcagtc agcgacaagg ctcccagccc tgccaccctg ccagccacct      60

cctcctccct gcccagccca gccaccccat cccatggctc tcccagttcc catgggcctc     120

cagccaccca ccctacctcc cccactcccc cttcgacagc cagtggggcc accacagctg     180

ccaacggggg tagcttgaac tgcctgcaga caccatcctc caccagcagg gggcgcaaga     240

tgactgtcaa cggcgctccc gtgcccccct taacttgagg ccagggaccc tctcccttct     300

tccagccaag cctctccact ccttccactt tttctgggcc cttttttcca cctcttctac     360

tttccccagc tcttcccacc ttgggggtgg g                                    391


<210> SEQ ID NO 198
<211> LENGTH: 563
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
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```
<221> NAME/KEY: misc_feature
<222> LOCATION: (116)..(116)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (168)..(168)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (175)..(175)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (225)..(225)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 198

agaggcaggc atagaggctt ctccgccagc ctcctctgga cggcaggctc actgccaggc      60

cagcctccga gagggagaga gagagagaga ggacagcttg agccgggccc ctgggnttgg     120

cctgctgtga ttccactaca cctggctgag gttcctctgc ctgcnccngc ccccnagtcc     180

ccacccctgc ccccagcccc ggggtgagtc cattctccca ggtanccagc tgcgcttgct     240

tttctgtatt ttatttagac aagagatggg aatgaggtgg gaggtggaag aagggagaag     300

aaaggtgagt ttgagctgcc ttccctagct ttagaccctg ggtgggctct gtgcagtcac     360

tggaggttga agccaagtgg ggtgctggga ggagggagag ggaggtcact ggaaagggga     420

gagcctgctg gcacccaccg tggaggagga aggcaagagg gggtggaggg gtgtggcagt     480

ggttttggca aacgctaaag agcccttgcc tccccatttc ccatctgcac cccttctctc     540

ctccccaaat caatacacta gtt                                              563


<210> SEQ ID NO 199
<211> LENGTH: 591
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(84)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(146)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (182)..(200)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (453)..(478)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (495)..(536)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (540)..(554)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 199

ctggagagcc agtgcccatg gcccgctgcg tctccacagg gggtcgcccg ccagcccaan      60

nnnnnnnnnn nnnnnnnnnn nnnggatgc ccaatacgag ccaggtgcca gggttcctgt     120

cnnnnnnnnn nnnnnnnnnn nnnnnntgga tattggtgcc ctcaagccag gtggacggca     180
```

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```
annnnnnnnn nnnnnnnnnn gagcacgaga gctttgagaa gcctcagctg ctgactgtga      240

acctcaccgt gtactacccc ccagaggtat ccatctctgg ctatgataac aactggtacc      300

ttggccagaa tgaggccacc ctgacctgcg atgctcgcag caacccagag cccacaggct      360

ataattggag cacgaccatg ggtcccctgc cacccttttgc tgtggcccag ggcgcccagc      420

tcctgatccg tcctgtggac aaaccaatca acnnnnnnnn nnnnnnnnnn nnnnnnnntg      480

ccctaggagc tcgcnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnagcn      540

nnnnnnnnnn nnnncatgtc tcctattcag ctgtgagcag agagaacagc t               591
```

```
<210> SEQ ID NO 200
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

catcagattt ctgcagatct gctttaaagc tgtacatttt tgttacagtc taagatgtgt       60

tcttaaatca ccattccttc ctggtcctca ccctccaggg tggtctcaca ctgtaattag      120

agctattgag gagtctttac agcaaattaa gattcagatg ccttgctaag tctagagttc      180

tagagttatg tttcagaaag tctaagaaac ccacctcttg agaggtcagt aaagaggact      240

taatatttca tatctacaaa atgaccacag gattggatac agaacgagag ttatcctgga      300

taactcagag ctgagtactg ctccagggtg gtgtgcaatc ttatattgat gcttgtgaat      360

ctgccatttg atttgtagga taaataaata tgtttaatat taacaacttc catcaaaact      420

ataataataa tattatatct actgttgacc tctaacaaca atcaggtgct gtattcagag      480

tcata                                                                  485
```

```
<210> SEQ ID NO 201
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

gccctgactg actgtattct ctggccacat tcaagtcccc cattggtggg ggcagagaag       60

taggaccagg ccatccttgg ctccagagct cgaagacccc aagacagccc tctgctctca      120

gcggcgccac agagagcctg ggctcagcct tctgcatcag gacatggcct cgtccactga      180

gggcacgatt taaacatttg acatcagaag ctttatttgt aaacctcaca cagataagga      240

ccaagggctg gcggtgtggc cagaggacag gggaagctga aggccccgtg cttgagctcg      300

gcagtcctgc tccttgcagt gaagccacca tgggtgaccg tccagcctca cccggtggcc      360

tgcacagtga gggaagggct tcagggccat ctgctcccag ggcagggggac aggccaccaa      420

ggacctttgg ca                                                          432
```

```
<210> SEQ ID NO 202
<211> LENGTH: 499
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (425)..(425)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 202

ggtggagaag ctggcgcgtg agaacagcag catgcggctg gagctggacg ccctgcgctc       60
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caagtacgag gcgctgcaga ccttcgcgcg caccgtggcc cggggacctg tggcgccctc        120

caaggtggcc accaccagcg tcatcaccat cgtcaagtcc accgagctct cctccacctc        180

cgtgcccttc tcggctgcat cctagtgccg gccggggggcg ggggtggcg ggcggcgggc        240

ggcgggcagg cgggtggggg cacacccctc gtacctgtca ctgggatgca gactctcgac        300

atccgagtcc aagcgcaggc ccctcgggcg caggcagctc acaccaggaa gagactgtat        360

tgcagggtga agagtgggct cccgtgggcc cagagctgca cgccggtcca cagacacact        420

cacgnccgcc acctgctccc cgcagatgtg tctgtgtgtg ggaattggta tcttgcaccc        480

gtgggagtcg ggacatata                                                     499
```

```
<210> SEQ ID NO 203
<211> LENGTH: 569
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (107)..(107)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 203

ttccagcacc attcttttcc tattaaatta cactggcaaa tttgattaaa aaaaacaact         60

gactatatat gcttgtaaac atttccagat tatgttattc ttttaancta aatatgtgtc        120

cttatgccaa taccccactc catctattac tgcagtgtat gataagtctt gaaatctagt        180

agtgtaagtt cttcaacgtt gcccttaatt tttaaaatca ctcttgctat ttaaaattgt        240

ttgtattaca tggaaatttt ataatcagct tgccaatttc tacaaaagtc ctgctgagat        300

tttaattggt attttgcttg ttctgcagct taatgcaaga aaattatctt aacaatattg        360

aatttttcaa tctattaaca tgttatatat tactgtttac ttaggatttt ttcacttttc        420

ctgccttgtt ttgaactgat attgtggttt taagtaattt tttttatttc tactattggc        480

ttagtaacta tgccccactt tttgattttg tagcacagtt gaccattgaa caacacaagt        540

ttgaattgtg catgtccaat tgtctatgg                                          569
```

```
<210> SEQ ID NO 204
<211> LENGTH: 266
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

ggagcagaga cagagcgacc catacctggc ccaggccccg gccccgcagg cagctgaatt         60

cctgagccca gtgacaaccc cttcccctg cactctgtcg tccgcccaag cctcaggccc        120

tgaggctgca gatgagactt gtccccagct ggctgtccat cctcctggtg tcagcaagct        180

gggtttgcag tgtcttccaa gcgacggtgt tcagaatgtg aaccagtgac tctcgggcgc        240

ccctgtggta actttgcagg cggccc                                             266
```

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<210> SEQ ID NO 205
<211> LENGTH: 506
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (99)..(99)
<223> OTHER INFORMATION: n is a, c, g, t or u
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (103)..(103)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 205

gcaagagctt tatccagagc tcccacctga tccgccaccg nccgcatcca cacgggcaac      60

aagccgcaca agtgtgcggg ctgcggcaaa ggcttccgnt atnaaaacgc acctcgcgca     120

gcaccagaag ctgcacctgt gttaggggct gggtccgcgg gaggctgccg tctgggggagc    180

ctgtgggggg tagatatcct gggactgacc caggggaagg aagtggggaa ggggcgggag     240

ggacaatctg agagtgactg gggagccttt ggtgtttggg gtttcctgaa gtgggaggag     300

tgttgagtaa gttggtcttt cccggtgcta tacttgcctc ctctccacgg aagaattgtt     360

caggagatgc gcttggggtg atgacttcct taaatacacg ctgtaggggg tgaagagctt     420

ggaggaccag gcactttgag gaagggcagt tcgtgggctg gggtgggaac aggatggcgg     480

gcaatagact agggtaggcc gcgatg                                          506


<210> SEQ ID NO 206
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(57)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(62)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (64)..(64)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 206

tcatttagcc ggtgtccact aactcagtgt tgtgggccat ttgtaaaccc ttntgnngtn      60

nncnccaggc agacgtaggg aaagaaagag aggatctgta tagacaagaa agctggccat     120

gtgggaagtc cagagctcaa accatgtgcc ccagaggact ggtgctggca ttaagcctgt     180

aaatcaaagg cttctttggc aggaccctgg gctgttagaa tcaccctagg gagcagagcc     240

aggggacatt ttggcccctg actagcaagg cacaaccctа taatggcaga agcccttctt     300

tccctcccc gtttcccacc agacccactt ccttgatggg cctctagcac ccttccaagc      360

tgatggggtc gggaatgtga gctggtaaaa tgggcagtgg aagggctgt actgtttctt      420

tacatctcac ggggactag                                                  439


<210> SEQ ID NO 207
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 207

aagaaatgct acctcggtgc catgttctgg actccgcaga acaaggactt tttggagaac      60

tccagcctat accctctatt gccatgacca gtacttcagc cactctggtg tcatctcagg     120

ctgatctccc tgaattccac ccttcagatt caatgcaaat caggcactgt tgcagaggtt     180
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ataaacatga gataccagcc acgaccttgc cagtaccttc cttaggcaac caccatactt      240

attgtaacct gcctctgacg ctactcaacg gacagctacc ccttaataac accctgaaag      300

atacccagga atttcacagg aacagttctt tgctgccttt atcctccaaa gagcttagct      360

ttaccagtga tattt                                                        375


<210> SEQ ID NO 208
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 208

gttcttgagt acatagccaa tgccaatggg agggatccca cttcttaccc atccctgtat       60

gaagatgctt tgagagagga gggagaggga gtctgagcat gagatgcaac cagggccagc      120

gggcagggaa atgggccaat gcatgcttca gggccacacc cagcagtttc cctgtcctgt      180

gtgaaatcag gcccattctt ccctctgtgt ttgatgagag aagtcagtgt tctcagtagt      240

agaaggcaca gtgaatggaa gggaacacat tgtatactgc ctttaggttt ctcttccatc      300

gggtgacttg gagatttctt tttgtttccc tttggtaatt ttcaaatatt gttcctgtaa      360

taaaagtttt agttagcttc aacatctaag tgtatggatg atactgacca cacatgttgt      420

tttgcttatc catttcaagt gcaagtgttt gccattttgt aaaacatttt gggaaatctt      480

ccatcttgct gtgatttgca at                                               502


<210> SEQ ID NO 209
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (110)..(110)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (114)..(116)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (118)..(119)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (127)..(127)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (129)..(129)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (131)..(132)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (135)..(135)
<223> OTHER INFORMATION: n is a, c, g, t or u
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (145)..(145)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (152)..(152)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (154)..(154)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 209

tcccctagct tggggtccag acagcccagt ggacccaggc gcctgagcag gagggtaacc      60

caggccaccc ggccccttcg gccctctcgg ccccaccccc tgcagccggn gncnnncnnc     120

nncnacnana nngcngcgag aagangacag angngactga gcaaaggggg gtgggctcca     180

ggcgacccct agcccaattc tgcccctcca tcccaggggg cagagaaatt gtctttcttt     240

gctgactcct                                                          250


<210> SEQ ID NO 210
<211> LENGTH: 440
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (142)..(144)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 210

tttggacatg tccattttgg aagaaacttt tgtgttaaaa taaactaata tattatgggc      60

tagaacataa aattcaccaa gaatttcaag ataaaaatac taatgttttg cttgtttggg     120

ttatttcaaa caataacttt gnnntctata attttttcac caccgaccct ctacctcctt     180

gcatgctcat tctcctgtgt ggctagatgc atttcgggtg ttttgaatat tatttcagag     240

caagtatcat tccagaaaat aagtttaaag tttgaaatgt ttattttttg taacccatga     300

atcttcagct taagtatctt ctgacataaa agcattttca taattataaa agtgctgata     360

ttactctcca cagtattata tctgatcctg caaagtagtt cagataccag agaatactct     420

taaacatttt gactcacgca                                                440


<210> SEQ ID NO 211
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 211

ggactcaggg agtacacact taccagtgcc cttaaagata gccgttttcc cccaatgaca      60

agggatgagc tgccacggct tttctgctca gtgtctctgc tcactaactt tgaagatgtc     120

tgtgattatt tggactggga ggtgggtgta catggcatta gaatagaatt catcaatgaa     180

aaaggatcaa aacgcaccgc cacctaccta ccggaggttg caaaggagca aggatgggac     240

catatacaga ccatagactc cttattgagg aaaggaggat acaaagctcc gattactaat     300

gaattcagga aaaccataaa actgaccagg tatcgtagtg aaaagatgac cctgagctat     360

gctgaatacc ttgctcatcg ccagcatcat catttccaaa atggcattgg gcatcccctt     420

ccgccataca accattattc ctgacactga gccgcacaac cagtcactgg gcctctctgc     480

agacctcttc ccaggagacc ctacaccttc ttggtctagc tatctctttt actgtaccat     540
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tttatgatga tagtttccgt tgccatggtg aag                              573


<210> SEQ ID NO 212
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 212

cgtccttgtc atatcctttt aactaggcat ctcagagaag cagagacagg gcagccttcg     60

tcctggggga aaagggaccc tcaggatggc atgagaggtc ctcaatccca agtgtggaac    120

tgtccccctc aacttgttaa aatgcagatt tctgggtctt gccaatgggg cctgggactc    180

catgtgacaa ctggcccagg agcttctgat gtcacacaga attctgcagt cccaagctcc    240

agccccgacc tgctctgctg ttcctaggtg actgccctca cactgctgac cacagtggat    300

ttctcccct gctgctcggg ctcagctggg gtcagccctg cttataaggt caactgtgca    360

aaaccttata ctggccaaga acaaactagt gctggggggag gagggctggg tgccccggcc    420

actggtggag tccccaggaa atcctcagag ctgttgcgag gatgagacac atttgtggac    480

acgtccacct gtcctcctga ccgtctggag agaa                              514


<210> SEQ ID NO 213
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 213

ccggctatgg gctcgagccg agttccttca acatgcactg cgcgcccttt gagcagaacc     60

tctccggggt gtgtcccggc gactccgcca aggcggcggg cgccaaggag cagagggact    120

cggacttggc ggccgagagt aacttccgga tctacccctg gatgcgaagc tcaggaactg    180

accgcaaacg aggccgccag acctacaccc gctaccagac cctggagctg agaaagaat    240

ttcactacaa tcgctacctg acgcggcggc ggcgcatcga gatcgcgcac acgtctgcc    300

tcacggaaag acagatcaag atttggtttc agaaccggcg catgaagtgg aaaaaggaga    360

acaagaccgc gggcccgggg accaccggcc aagacagggc tgaagcagag gaggaagagg    420

aagagtgagg gatggagaaa gggcagagga agagacatga gaaagggaga ggaagagaag    480

cccagctctg ggaactgaat cagg                                       504


<210> SEQ ID NO 214
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

gaaattattc actccgtata ctgaaacaga aataaacgag gaagaactta caaagccaag     60

actcttgtgg gctctttatt ttaatatgag agattcctcg ggaatcagca gaagctcgta    120

taatggcttg ccttccaatg tttatgtctg ctctgggcct gactgtggcc tgggaaatga    180

gcatgctgtc aagcaagctg aaacactttt ccaggagatc tttccaactg aagaattctg    240

ccctccacct ccaaatccag aagacattat ctttgatggt gatgataagc agccagaggc    300

tcctggaacc aataatgtag taatggccaa actagaatcc tctgaggaaa gcaaaaacct    360

agaaagccca gagaagcacc ttcaaaatta gaaagagca atctcgaaat gctgttttgg    420

acctccttca tggcatcaga attttctcat ttaaaggaca gtttcccata tgagtaatta    480

gaagtggtta tatatgatga atgctatgca gatgttgtct ttaactctc                529
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<210> SEQ ID NO 215
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 215

tctttgctct agtattccac ggtgcctctg acatgagaac aggatggaga ctggcttctg        60

atttgacatg cattttgtag gtatgatcca aaatagcttg gaaactatcc cagtcttcaa       120

ccatcccatt ttttagaggt gaaatggcct ccatattctc cctcggaaca cgcagagcat       180

tagtatctat gtagtaggtg ggaccgcctt gtttgccttt atcgccatct atttccatta       240

atgtgcttcc gtcatctctt tctaccacca taccaatagc tgtaggaaaa tccaccttgg       300

ggcagtcctc accagcataa ccagctctca cagtatagga tccaatgtca aaaacaaggg       360

ctccaacttc atctcccccg taccacgccg ccgctcatgg ctgctgccgg cgcgactcct       420

accctaaggg ctaactggcg aagtgactgc agtggccgcg actgcgagtc tcgaggagcg       480


<210> SEQ ID NO 216
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 216

tggaagcatt tgttgcctcg atcttccact ttagaaaaat gaagtttctc cttttctttg        60

ggagaggata tatctgaata cttgccttct tggcatttat acattcaaag ctcagtgcta       120

gattagagct attatttgca tagtcttttg gtattgccca cttttggcat taccatatta       180

tttgacaatt agaaggaata gggaaggaat attacatgac tgtaaaagag ttggttatat       240

tttatgttga cttcaagggt tccatttgaa ctattatggg ca                         282


<210> SEQ ID NO 217
<211> LENGTH: 563
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

gcaggaccac cttgaattct gccctgacac actggattgg agagcagcag aacccagggc        60

ctggcccacc aagctggagt gggaaaggca caagattcgg gccaggcaga acagggccta       120

cctggagagg gactgccctg cacagctgca gcagttgctg gagctgggga gaggtgtttt       180

ggaccaacaa gtgaccactc tacggtgtcg ggccttgaac tactaccccc agaacatcac       240

catgaagtgg ctgaaggata agcagccaat ggatgccaag gagttcgaac ctaaagacgt       300

attgcccaat ggggatggga cctaccaggg ctggataacc ttggctgtac ccctggggga       360

agagcagaga tatacgtgcc aggtggagca cccaggcctg gatcagcccc tcattgtgat       420

ctgggagccc tcaccgtctg gcaccctagt cattggagtc atcagtggaa ttgctgtttt       480

tgtcgtcatc ttgttcattg gaatttttgtt cataatatta aggaagaggc agggttcaag       540

aggagccatg gggcactacg tct                                              563


<210> SEQ ID NO 218
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 218

gccagacaac ctgagtgtga atccagcttc accacttcat tcattcactc acccattcat        60

tcaacaacat atttgaagca catactttgt accagggacn tttccaggca cnggactaca       120

gctatgaaca agacaaacag tccctagcct cccaagagcc gtcacttcag aagggcagac       180

atgacacgca aacaaaatga tgccaggtgg taccaagtgc cttggggaaa cagtgccacc       240

tttctgagac cgtttctcca tccgtccatg gagctgataa caccagtccc tcagggtgga       300

ggtgaagact aagaggttgc tttgagaggg ggaacttggt ggctttttt caccacctag        360

aacctggcac atactaagct ctcaataaaa g                                      391


<210> SEQ ID NO 219
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (417)..(417)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 219

aactacgcct ggtacaagct ggcagaggag gtttctgggc gcacagaagt cactgtgaaa        60

cagccagaca gccgcctgag gctcagccaa gcccagggga acctgtcggt tctggagacc       120

cggcaggtac agctggagtg tgtggttctc aaccgcacca gcataacctc ccagctcatg       180

gtggaatggt ttgtatggaa gcccaaccac cctgagcggg agactgtggc ccgcttgagc       240

cgtgacgcca ccttccacta tggagagcag gcagccaaga acaatctgaa ggggcggctg       300

catttggaga gtccttcccc cggcgtgtac cgtctcttca tccagaacgt ggctgtgcag       360

gacagcggga cctacagctg ccatgtggag gagtggctgc ccagccccag tggcatntgg       420

tataagcggg cagaggacac cgctgggcag acagctctga cagtcatgcg acca            474


<210> SEQ ID NO 220
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (125)..(125)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (133)..(133)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 220

gggaccttgt aacttccttg caagttaagt gagctatcct gtcacggttt tatgttgagt        60

gagtgggaag ctgggactct gttttacagc catctgtact ggagcctgga caaaccactg       120

gtctntatgg gangccccag cctcacattt ccctggcaag gagagagagg tttagccatg       180

tcctgggtct aggattacag cccagagatg ggcacttaag aagacctggt cattggtcca       240

gacttgggcc aaggctctcc tctgtgaggg atgggtttta ctggtgaatt acctgtgtgg       300

agaagctatc agggccatgt ttagcacact gaagggacca gtctccacca agcactttaa       360

catccctcca gccagcatag attgatctcg tgttacagag agggcaaggt ttttggcccc       420
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tgtttgcaga ctccatgtct taatcagaga ccacagtttt ctctttgttc c   471

<210> SEQ ID NO 221
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (408)..(408)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (439)..(439)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 221

taaataatgt cctctacgtg ccggtgtgga agtagcccgg atgcaattga atgaacaaca   60

gacggtgctt tccaggacgg cgctgtgctt tccaggatgg tgctgtgctt tcattcattt   120

gggtagctcc tctgtgagcc tcccagcgcc gactgcagag cccccactct ccagcctgca   180

agaccccgaa attcaagcca cacaaagaaa ggaggagggg gccgttggca tttactgaac   240

cttataaaac tgtcagcaaa acagccctta ggcttggact ccctgctagc cgggtttttac   300

ggtgctgaag tcagcatctt gattcagctg cataaataat ctcctgcagt cctgcaaggc   360

ctggggtagg agagggtatg gggaccaggg cactctgtaa gggctggnat aggaacccca   420

gggaataaga cagaccaant gcgggacttc agactccact gcagccggga tcgggttgtt   480

gttaatttct taagcaattt ctaaattctg tattgactct ctcatgc   527

<210> SEQ ID NO 222
<211> LENGTH: 310
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(43)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (110)..(110)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (115)..(115)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (189)..(189)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (236)..(236)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (252)..(252)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 222

atacatgtgg ttatcttttg ccctgttgtg atggataatt tgnaaagaag tgggtttatg   60

tcaccttctc accttcttat aagaaagctc tgagaatggg catttttgtn ttttnttgtt   120

gttgttgaga tggagtctgc cacccaggct ggagtccagt ggcgtgatca tacctcactg   180

cagcttcanc ttcctgggct caagtaatcc tcccacccca gcctcccagg tagctngtac   240

tataggtgtg cnccaccacg cccagcaaat ttttaaattt attatagagt gggaggcagg   300

```
gtgcggtggc                                                             310


<210> SEQ ID NO 223
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (169)..(169)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 223

cactgtctgt gtgagtccat tcacttcaat accagagcca cctctttgtt tcctatttac    60

taagaagcca taccagcatg agatctcctt gatagtgtta aatcccactg tggaaagatt   120

gaaaaatatc tcccagcctt accagaggtt acgatctagt gtggaggcna aagacattga   180

gaagaaaaaa gcaggtgcct cctcctggct ctcctgttag gttaacataa tcataattcc   240

cctttgaaat gtctcccaca tttgcccttt aacttcctat tgc                      283


<210> SEQ ID NO 224
<211> LENGTH: 499
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 224

gacgactacg gtctggacaa ctttgacaca cagttcacca gcgagcccgt gcagctgacc    60

ccagacgatg aggatgccat aaagaggatc gaccagtcag agttcgaagg ctttgagtat   120

atcaacccat tattgctgtc caccgaggag tcggtgtgag gccgcgtgcg tctctgtcgt   180

ggacacgcgt gattgaccct ttaactgtat ccttaaccac cgcatatgca tgccaggctg   240

ggcacggctc cgagggcggc cagggacaga cgcttgcgcc gagaccgcag agggaagcgt   300

cagcgggcgc tgctgggagc agaacagtcc ctcacacctg gcccggcagg cagcttcgtg   360

ctggaggaac ttgctgctgt gcctgcgtcg cggcggatcc gcggggaccc tgccgagggg   420

gctgtcatgc ggtttccaag gtgcacattt tccacggaaa cagaactcga tgcactgacc   480

tgctccgcca ggaaagtga                                                 499


<210> SEQ ID NO 225
<211> LENGTH: 562
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 225

tcttctgtgg aggaatggca tcccaggcct tcacccctcc aggtcagccg tggctgccgg    60

ccaagatggc cgcgtgggca gcctcacatt ccttctcggc ttttggcccc atgtcctcgg   120

cactcaggtc tgcagttcag cccaagtgtt gagactcagg tatgcagctc agggcggcct   180

taattaaccc tcccatgggc ctgggcaccg cctgcgcctc atcaactctg ggctgctggt   240

tttgttcctg acgctgcagc ctgacactgt gggcgggggt gcagtttgcg atggaaggct   300

gcctccgaat cgaggaagcc ttgaccttgg gaggggcctg cctttctcgct gggcttgcct   360

ttctctgggc agcgttcgct cagcacttca gtgcggccga ttccctgggg actgaattca   420

caccagccac gacgacttcc cggctacttc acgttctcta tgtttgcagc tgttctttgg   480

tggcagaaaa agatgatttt tcttccccc actcccattc ccttttgtta gtttctctcc    540

ctgaaccaca ttttgagctg ag                                             562
```

<210> SEQ ID NO 226
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 226

ttccagaatt tcttccgagg tagtatggtt ttcttcatag gataaag   47

<210> SEQ ID NO 227
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (476)..(476)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 227

aggcagcgct gcggagagga gcggcagagt gggttgtctg ccgcaggcaa ccaggcaagt   60

gtgtcggggc tggggtgtga atgccagcct gtgagtcccg gaactatgtg ggtacccta   120

cccctcacag aagccaaggg catggaggag gtccctccac agtgacaacg gtgtggggta   180

ggggaggtgc attcaggaca ccacccaggg acagtgccta tgtgatcacc tcttaaaggc   240

taagcttagg ggcatttccc aaagtgggga cagagggcag gacgcccagg ctgggggctc   300

tcctcgcccg ccctggtgtc tgacagcctc aaggaaggag cagtgcctgt gtcagccatg   360

gggcccttgg agctgccgct ggtgcctagg gggcctgggt ttctgcccag gcagccagtg   420

gctgttggga gcctctgttt cccctgtgct ggggccttg agtgctatgc tagcangggc   480

ctggccccaa gtgtgagtga tgagcaataa acgtaccgtc ccc   523

<210> SEQ ID NO 228
<211> LENGTH: 138
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 228

aagtgcgaag tcagggatgg tctaagaggg ctgagaggag aattccggaa cctcaggacc   60

ttgctcactg gctgctggct ggggctgtga agctgtccag tctagaactc aaagagtgat   120

ggtacaggct ttagagcc   138

<210> SEQ ID NO 229
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (198)..(198)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 229

gggctgggta cctcttctgg ttgctgagtg gagtgcacca gcagccccac cccagagaag   60

ccctgttgga agcgctgtgg gaatccccca aggtagggga gtggacacca taaggaaggg   120

gaggagtgcc agctccatat gcggtctccc ccatcagtca ggccagcagc gggttcagct   180

gcctctgggc agccctancc catacagaca gggagacctc cctcccgatc ttctgtgaat   240

agtcccttat acccctgctt atgcctcagg ggctcctcca cccttttgtc ttcatactgc   300

atatgaaaac tgcccttgta tatgtggata tctgaatgtg tcagtgaagg cctatatgaa   360

tgtgcacatg tgggtatgtt ctcagccatg tgtata   396

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<210> SEQ ID NO 230
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 230

gaactaaagg agccatctct ctccctctc ctccgttcnc gagaggaggg gtgggtctca      60

gacgtttttc ctatggactt atttcttcca tgtccaggac tttgcacaac tttggtttta     120

aaagctgttg aaaaatagga aaacaaaggg cattgttcac agatagggcc aagtctcccc     180

ttgcaagggt gcctctgttc tgtccctgcc cccacctcac cttctctact cctccagtaa     240

gttggcagtt ttggtgccaa accccaaatc tccaaagaga catgccaggc aagacaaacc     300

cccaaacacc tcctttccgg tggccttgga aacagattgc tccgagctgg agaatgtcgg     360

gtgaggtgta tgggagagga ggggagagtt agaacttgtg cctttgggag taaggggtaa     420

ctgcctggag gg                                                         432


<210> SEQ ID NO 231
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

atcagtgcca gaaattcctt acctaaagtg gcatatgcga cggccatgga ctggttcata      60

gccgtctgtt atgcctttgt attttctgca ctgattgaat ttgccactgt caactatttc     120

accaagcgga gttgggcttg ggaaggcaag aaggtgccag aggccctgga gatgaagaag     180

aaaacaccag cagccccagc aaagaaaacc agcactacct tcaacatcgt ggggaccacc     240

tatcccatca acctggccaa ggacactgaa ttttccacca tctccaaggg cgctgctccc     300

agtgcctcct caaccccaac aatcattgct tcacccaagg ccacctacgt gcaggacagc     360

ccgactgaga ccaagaccta caacagtgtc agcaaggttg acaaaatttc ccgcatcatc     420

tttcctgtgc tctttgccat attcaatctg gtctattggg ccacatatgt caaccgggag     480

tcagctatca agggcatgat ccgcaaacag tagatagtgg cagtgcagca accagagcac     540

tgtataccc                                                            549


<210> SEQ ID NO 232
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

gatgagtcca tctcacttgc tcagaacttt gcctggtgag agcggttaca agcgaacaag      60

gtggaaatga aagaaaccct gactttccca ctaggaagga agagactgtt ccttcttgtg     120

atgtactctg aagaaaaatt ctaggatttg gacagatttc ttgggttata aaacatgatt     180

ttcttctctg tttcttgggc ttttataatg ggtactgttg ttttcttgca aagctttaat     240

gattccataa ggacttgtat aaagtttatg ggagaatttt caatgtagat gtgaatggca     300

gaaacccaag aatctgtgtg aggttgaata agatcctgtg tctccagaga ggtctgatgg     360

ggagacacag atctaaattt taaaggtggt ttggccttc tcaatcatat attaaggtcc     420

ttttatgtta tagataagta aattaaggcc cagaaagatt aatagcccaa ggtcccaaga     480
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cctgcttgag acctgtgccc catttctgac taatattctt catgatattg tatcactctg        540

tatcaaaacc aacc                                                           554
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```
<210> SEQ ID NO 233
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

gatggtgcag tacctgctag cactttgctg cagaatgcct ctgcactcag ttctgcaaat         60

gtactgtttt agtttcattt aaaacccctt tttttgtgag aagatttcaa acatcaggca        120

agtttgtaat gaattcaagc tgagttctct cgagggacaa acatgtataa ctacagttcc        180

agtgtcagtg ccagctgtca ggttttcact gtgcagctag ggctgcctgc atacccagtc        240

atgtaaacca aattcactct agaatcggcc aggtcttacc aaaatgcaaa tagaatacaa        300

agcaactgga aatatatttc gtaatttcat tttatgtgtg attttaaaag ttaagctact        360

tcaaaactca tctgtctaac ttattttcac taataagtgt aacttgcctg gaatttggca        420

gatctaagct gggcttgggc tagatggttt caagcctgag tcattaagat gtgaaattta        480

cagaaacaac agaggattga ggaacaagtt aaaggacact ctaatggtgc agtctgcat         539
```

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<210> SEQ ID NO 234
<211> LENGTH: 431
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 234

gtgagcatgg aagtagatct tccccggtca agcccccaga aggacccagc cctgcggaca         60

ccttgaccga aacctgtgag agctccggaa atagaggaac cnagcattcc ctctggaata        120

catcagcact gttgcctttg aggctggcct gcttgaatgc acacctgagc tccggattca        180

cagtggagga agccagatgc catgtcatga gggtgctcaa gcaacttttt ggagatgtat        240

gtatggagag aaactgaggc ctcctgccaa cagccagcac taacttggca agcatgtttg        300

agagccacct gggaagtgga gccttcagcc ccagttaagc cttcagatga gactgcagtc        360

ctggccacca tctggactgc aacttcacaa gagctcctaa gccagagcca tgcagatgga        420

ttcttggccc c                                                             431
```

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<210> SEQ ID NO 235
<211> LENGTH: 403
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (139)..(139)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 235

gatctcattg ccttttttatg ccgattaaca tgcttttagc ccctactgag cttatagtta        60

acagaagttt ccaggtcttt cttcacctga actgtgtcta aagcaagttc cctccacctt        120

ctgtatttat acgcttgant ttttaaaacc taaatgttgg gcttcacatt tgttccttgt        180

aaatttcatc ttggtgattg cagtctaccc tctggccttt aaaaattgtc tgagccttga        240
```

```
ttcgatcatg aaaccagctt acccttcccc tgtgtgctgg ccccagtttt ctaaccaggt      300

gttgaatgaa ctggatggac tctgccagat ccctccgtgc aaggctggaa tcagtccatt      360

gttcaactgt gccctttggg gctgtggttc atttggctct gat                        403


<210> SEQ ID NO 236
<211> LENGTH: 257
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

ctgctggaaa ggcatccttg ctgcagctgt gagtgtgatg ggacagcaga gtcactcctg       60

catgggattc tagggctggg ggtcccagag gggtggcctc cgccctcct ggggccgag        120

gactgtcacc atgtcactac ggcactctcc agctgctgac caaagccctc gctaaccgca      180

gccctgccat actctgggtc tttcctctgg agcaaggtga agagactgca gcgaggcgtg      240

gaattgggaa gctcttc                                                      257


<210> SEQ ID NO 237
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 237

actgtgactg cgcgcaggac gagaactgca agtccaccaa gcgcgccatt gagccgtgcc       60

tgccccggac gagcggcggc ggcgcgggcg ccccggcgc gggcggggtc atgggctgca       120

ccgaggcccg gcgccgctgc gaccgcgaca gccgctgcaa cctggcgctg agccgctacc      180

tgacctactg cggcaaagtc ttcaacgggc tgcgctgcac ggacgaatgc cgcaccgtca      240

ttgaggacat gctggctatg cccaaggcgg cgctgctcaa cgactgcgtg tgcgacggcc      300

tcgagcggcc catctgcgag tcggtcaagg agaacatggc ccgcctgtgc ttcggcgccg      360

agctgggcaa cggcccccggc agcagcggct cggacggggg cctggacgac tactacgatg      420

aggactacga tgacgagcag cgcacc                                            446


<210> SEQ ID NO 238
<211> LENGTH: 340
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 238

ggaacagagg agagatgccg gctggaggac acagcaaatt tgaaccaaga ggagcttgga       60

ggaagcccga gcgacctgga ggggactggc tgaccttcct cattctttc aagtgtgaat       120

aataaccaag cccagtttgg caactccttg agggtgagga cgaagcccca ttctcctttt      180

tggaacttgg tggggctcag gaagcaggtt ctctccagtc ggtggctttc ctttctgttg      240

cgggtctctt gagggcctgc cttcatgaag gcacatgagt gactcatcat ttgtgaatta      300

attgctatat gtgaagggca tctgagaaca aattatcttc                            340


<210> SEQ ID NO 239
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 239

tgaccgccat gtggctgtgt ctgaccgcct gcgatactcg gccatcatgc atggagggct       60

gtgtgctagg ttggccatca catcctgggt cagtggctcc atcaactctc ttgtgcagac      120
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tgctatcacc tttcagctgc ccatgtgcac taacaagttt attgatcaca tatcctgtga      180

actcctagct gtggtcaggc tggcttgtgt ggacacctcc tccaatgagg ctgccatcat      240

ggtgtctagc attgttcttc tgatgacacc tttctgcctg gttctgttgt cctacatccg      300

gatcatctcc accatcctaa agatccagtc cagagaagga agaaagaaag ccttccacac      360

gtgtgcctct cacctcacgg tggttgccct gtgctacggc acaacgattt tcacttacat      420

ccagcccac tctggtccct cagtccttca agagaagctg atctctgtct tctatgccat      480

tgttatgcct ctgctgaacc ctgtgattta tagtctaagg aataaagagg tgaaggggggc      540

ctggcataaa ctattagaga                                                  560


<210> SEQ ID NO 240
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

ggaaatagtt tgttcatatg gccaaattat aaagggactt agtaaaagaa agctatgttt       60

tctgattacg aaggaaatct atgctcacag tgggaaaaca agaaatgtg gcaaagcaca      120

ggtaagaaaa taaaaatcaa taatatcaac attatgaata ttttaggtac ttaggaattt      180

ggggtagaat gatggaaagc aaactgttaa ttatagctgt atatttcagt gtagaggcta      240

caggtgcctt gcatttgttt tcttataaaa tctgttccca tacattttac ttactttatt      300

tgaatttagg aaactttcat taggtagcca ttttttatttt ctgtttcttt aatcatttta      360

ctttgaaata attttaaatt tacagaaaat ttgcaaaaat agtgtagaaa tttcccattt      420

gcctttatcc agcttcctgt agtgttgcca ttttatgtaa ccatagtaca attattgaaa      480

ccaagacatt aactttgaga ggctgctact actctaagaa ccat                       524


<210> SEQ ID NO 241
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (71)..(72)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (197)..(197)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (219)..(219)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (233)..(233)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (289)..(289)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (309)..(309)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (346)..(346)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (390)..(390)
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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (395)..(395)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (474)..(474)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 241

tcctgtgtct tgacccagaa aattgtgaca tgtaaaaaga ataaattcct ggtttaagcc      60

agtaaggtta nnggtacatt gttacatctc agataattaa aaccttgaaa aactcatgag     120

agatcacaag tagaaccttg atctgaaaca tggcatgtgg cgatttatat tgagtattag     180

gttaaaaatg caagaangga gcatagttaa tattttacnt taaagctaaa acnataattg     240

cctacttaaa attttcagtt aattaggttg tcactttttg ttcttaacna agaaatcaac     300

tagtttttant ccataaacag ttagaactga tgcacacatc cgtttntcct tactcatttt     360

aaacagctat ctgaaatagg aagtgtaatn taatntttaa agaatctgaa aacatgacag     420

aaatgtttaa actataaaca tatattgtat atgttagcat attgtataca ttgnatatta     480

acataagcta gaatcattga cata                                            504


<210> SEQ ID NO 242
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

cgaaccactc agggtcctgt ggacgctcac ctagctgcaa tggctacaga ggctggaaga      60

tggcagcccc cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc     120

acacaacgat gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat     180

ggacaaggtc gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg     240

cttctagctg cccgggtggc atccctgtga cccctcccca gtgcctctcc tggccttgga     300

agttgccact ccagtgc                                                    317


<210> SEQ ID NO 243
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

aatgccggct ggctcagtga tggctctgtg caatatccca tcacaaagcc cagagagccc      60

tgtgggggcc agaacacagt gcccggagtc aggaactacg gattttggga taaagataaa     120

agcagatatg atgtttttctg ttttacatcc aatttcaatg gccgttttta ctatctgatc     180

cacccccacca aactgaccta tgatgaagcg gtgcaagctt gtctcaatga tggtgctcag     240

attgcaaaag tgggccagat atttgctgcc tggaaaattc tcggatatga ccgctgtgat     300

gcgggctggt tggcggatgg cagcgtccgc taccccatct ctaggccaag aaggcgctgc     360

agtcctactg aggctgcagt gcgcttcgtg ggttttccag ataaaaagca taagctgtat     420

ggtgtctact gcttcag                                                    437


<210> SEQ ID NO 244
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (299)..(299)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 244

tagatcatgc cctcattggg cttacatgct gttgaaaaga taggatataa atccatgaaa         60

atttttacaa tgctatttat taacaataca tgacaagagt actagaaatg ttacttgtga        120

ctattttgtc tattctagcc aagctggatg cctggctgtt tctcagttat actaaatgag        180

ttctgctctc agggtcttca tacttgccct tccctctgcc tgcaacactc ttcctccagt        240

tttttttttt tttttttggc tctctccatc actttaggtc tccattaaaa ctgtcagcnt        300

tcagggaagt tgccttccct gaccacaacc acactaattc aaataccaat ccttccccgc        360

ctccgtttgg taactctcta gtctcttat                                          389


<210> SEQ ID NO 245
<211> LENGTH: 136
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(69)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (91)..(91)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 245

gccccaaggt ctttaagtat ctctgtcact tattagctca ccagagaaga cacaggaatg         60

agaggccnnt tgtttgtccc gagtgtcaaa naaggcttct tccagatatc agacctacgg        120

gtgcatcaga taattc                                                        136


<210> SEQ ID NO 246
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 246

ggccctgggc taagtcgggg atgaaggcgg gagctgctgt gctggactgc agctcagcac         60

agagacagtg agcctagatt gcagagctgc ccagggaggg atgtcacctt gggggatgga        120

ggctgcaggt gctcctcaga ccttagggaa acatttggga gggagcttgt tgaggagata        180

caggcacctc agggtggctg ggctggatgg actttgatga cccttccttt tttgagacct        240

gatggttctc taatttggga atcatttcca aagatgggtc taaaaatcct tgtttcattg        300

gaaataatga gtttgctatg atgcttaaga ccaagcatgt caccatttgt tattactgca        360

cttttccct                                                                369


<210> SEQ ID NO 247
<211> LENGTH: 444
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 247

gaggcttttg acacagttat tagttaaatc aaatgttcaa aaatacggag cagtgcctag         60

tatctggaga gcagcactac catttattct ttcatttata gttgggaaag tttttgacgg        120

tactaacaaa gtggtcgcag gagattttgg aacggctggt ttaaatggct tcaggagact        180
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tcagtttttt gtttagctac atgattgaat gcataataaa tgctttgtgc ttctgactat      240

caatacctaa agaaagtgca tcagtgaaga gatgcaagac tttcaactga ctggcaaaaa      300

gcaagcttta gcttgtctta taggatgctt agtttgccac tacacttcag accaatggga      360

cagtcataga tggtgtgaca gtgtttaaac gcaacaaaag gctacatttc catggggcca      420

gcactgtcat gagcctcact aagc                                             444


<210> SEQ ID NO 248
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

ggggcggcgg aagcgagtag agtttgtgac atttgtgcca gcccctccag cccagtcacc       60

tgaggagcct gtaggggccc ctgctgtgca gtccatcctt gtggcaggcg aggaggacat      120

ccgctgggtg tgtgaggaca tggggctgaa ggaccctgag gagcttcgca actacatgga      180

gaggatccgg ggcagctcct gaccctccac agccacctgg tcagccacca gctggggcaa      240

cgagggtgga ggtcccactg agcctctcgc ctgcccccgc cactcgtctg gtgcttgttg      300

atccaagtcc cctgctggt cccccacaag gactcccatc caggcccccct ctgccctgcc      360

ccttgtcatg gaccatggtc gtgaggaagg gctc                                  394


<210> SEQ ID NO 249
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 249

tttgctttgg gtactgtgat aactacttt tatactttat cccatttaat tataaaaacc        60

actcttgaga agtaattttt attttcagaa ccatttaca gatttaaaat aaacaggttt       120

gaggaattag tttaacttat ccaaagtttc gtggctatta agttctagta tttggagtca      180

aatgcaagtc tgtctaaatc tagagcccat gttctttaac tgcaacacta taatgtctca      240

ccccgtccta gtcccaccaa ttagtcaact ctttttagggc agaagtctgt ctaattcatc      300

tttgcttcct gttactttat atttaattaa aaattttagt gacttttaa cttgtaaatt       360

gtagctgatt ttacatttat cttcctgaag gaaactctgt atcattttgt cttt           414


<210> SEQ ID NO 250
<211> LENGTH: 268
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 250

cttttattag aatgccatgc ctgcttatgt tatgcatgta ttttataata atttaatcta       60

ttttacaatt ttaaactcaa atatgattta gtattatgca cataatacaa acagtagtgg      120

tgagcaaacg tgtgtttccc ccacatgtgc agaatatgat ggattttatg aaaataaata      180

ttcttaactc caggaaatat gatctatatg gttccttaaa agattttcca atacactgaa      240

aatttagttc cttatgttca ttgtataa                                         268


<210> SEQ ID NO 251
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (131)..(132)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (156)..(156)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (187)..(188)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (230)..(230)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 251

cgtgcagcag atcccaggag ttggaaaagt taaagctccc cttctcctcc agaagtttcc      60

aagcatccag caactgagta atgcttccat tggggaactg gagcaggtgg tcggacaagc     120

agtggcacag nnagatccat gccttcttca cgcagnccca ggtgagggct ggcctcaggg     180

ccacggnnat cttctcccga gaccacaaac accaggatct tgttttcagn tttaaaaacc     240

aagagaatgg gccgggtgca ctggctcacg cctctaatct cagcactttg ggaggccgaa     300

gacagcggat catctgaggt caggagttca agaccagcct ggccaacatg agaaaccccc     360

taaaaatagg aacaattagc caggcatggt gacaggtgcc tgtaatccca gctacttggg     420

aggccgaggc atgagaatca ctt                                             443


<210> SEQ ID NO 252
<211> LENGTH: 281
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 252

gagaaattcc cacactaaaa acactacaag ttttttggaat cgtgccagat ggtacccttc     60

aactgttaaa ggaagccctt cctcatctac agattaattg ctcccatttc accaccattg     120

ccaggccaac tattggcaac aaaaagaacc aggagatatg gggcatcaaa tgccgactga     180

cactgcaaaa gcccagttgt ctatgaagta tttattgcag gatggtgtct cttctttaga     240

acagggaaaa taggcaggaa gcccaattgc tggagtactt a                         281


<210> SEQ ID NO 253
<211> LENGTH: 249
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 253

ccaaatatct agattctgat ccctttgag gtcctagacc ctttgagaaa ctgatgaagc      60

caggcacctc cttcctcagg aaaatgctgg tgtacaaata cacacaaagc tcttcaggca     120

gctgatagat ttcccccaga gagctattca aggacttcct aaggtgggtg gactgcaggg     180

ttaggacacc tgctatagag gtgacatttt tccaaggaca agcagggact ttggtcttga     240

ctgttctct                                                            249


<210> SEQ ID NO 254
<211> LENGTH: 259
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 254

agaagagcct gaacctcaac atcttcctga agcaatttaa gtgctccaac gaggaggtcg      60
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ctgctatgat ccgggctgga gataccacca agtttgatgt ggaggttctc aaacaactcc      120

ttaagctcct tcccgagaag cacgagattg aaaacctgcg ggcattcaca gaggagcgag      180

ccaagctggc cagcgccgac cacttctacc tcctcctgct ggccattccc tgctaccagc      240

tgcgaatcga gtgcatgct                                                   259


<210> SEQ ID NO 255
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 255

aaattctgca atgaaccсta caccgaccgg acagaagaaa gggaagaatc caaagaggaa       60

gaagactggt ccctccgacc tgtcctttcg ggagctgaga aagatgacga agctgagcgt      120

ctcagagaaa caacagaaga cggagaagac ccgccaggct acaccaccga catgagaaca      180

gataaagaag ctgactcaaa tggcagaggg cagcctaaag gagaaacaac tggcaattat      240

cccgggtaat atgatcttgg ctgccttgat ggtaattacc gcggcggtaa gtctccctgc      300

tgtctggact gaagaaaatt ttacatactg gcttctgttc catttcctcc tttaattagg      360

ccagttactt ggatggattc ccctattgaa gtttatacaa atgatagtat tttggatgcc      420

tgggccgatt gatgatggct gtcctgcaca gcctgagaag gagggtatgt tgatgaatgt      480

aactggtatg aataccctcc aatttgttta ggaattgctc cttgatgttt accat         535


<210> SEQ ID NO 256
<211> LENGTH: 230
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 256

ggaagtaatg acttttttgc ccatttactc actgagtccc ataatgtggt aaatgtataa       60

tgctgacatt tgttccgtcc ttatagattg aggatagtac ggccctgaat tttgccttta      120

ctttagaaac ctgattcaac ttaaccgaac tctcaggaat ctgattccta agctgagtat      180

cacattttag attacttact aatttgtgca tctatccacc tagcaaatat                 230


<210> SEQ ID NO 257
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (152)..(152)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 257

taaaaccaac cagctgaacc tttcaggcta caagagaacc cgggtcggta atgtcttttt       60

aagaataatt tttaattgct tataacaagc atatttngtg gcatttgaac tatatttact      120

gctccaatat ccgttatttt ccaaaggatt tngtatcttt ttgaaaatgt ttacatcatc      180

agatgatcca cagaattcac tttatgtgag atctcccgag agtttccatc ccaacataat      240

ggactttggt ttgaacacaa ttcgtttttt catttgaatt ggcatttccc aatatttgct      300

aaacatttgc tggagaaatc attttttcttt tttctttttt agaaaactca gaatgaaaat      360

tcattcccct gaaatattta ggtgtctata ttctatattt tgatctatta agggattagt      420
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attttttccat gtttattgtg ttatcagagt gcattagaaa gattagtgat tcatcttcac        480

agcacatttt taatcaagca gttatttcaa ccagcacatt cgttttgttc at               532


<210> SEQ ID NO 258
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (363)..(363)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (441)..(441)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 258

atcacccccct gttcattatg tcaggcctca tgggagcctg gccttctcca gaagctggcc        60

ccggcgtcct cccaagctgg accacgtagg ccccagatca cacctggggg tccagatgta        120

ggggtcccgt gtgcacgccc aatcagaccg agcacttgtg acactacccc aacacctctc        180

ccagggctga atgaggaacg cgccactgga cacatgagga agaggctgcc ctgggagcta        240

ctgatgctgt gacctcacct ctctggcttt gggcggcagg tccctgcacc taggatgcct        300

gcctggaaat gtccttgcat tcgtggcctc cttcacagcc tcctcctcag agaagcctct        360

gcnagtgcac agggagtgtg tgcagccttg tgaagggctg ggaccacttg cccagactgg        420

ggcccctcag gcacaggcgt ngggtcctac tgacctgtct ccccagctcc cacacagaaa        480

gcatctaaa                                                                 489


<210> SEQ ID NO 259
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

cagaaggaaa cggtgtctct cggctgtggc tctgagtgca aattgcatgg gcggaaaggc        60

ggggggtggct gctcttcctg gcaggcctgg gccatcagcg aactgggccc cgtgaggagg        120

gcggggagtgt ggaggagggt gggcctctca cccaggcttt ctcggcccct ctcctcagct        180

tgcagagctg gccagcccccc tccttagggg gtgggcgagg agcctctggg cagacccaag        240

aaccatgggg actgggggtgg gttggtggca ccaatggcag ccctccccgc ccctctcctt        300

caaggagggt tcccgcagct gggggggtgtg cggaggcgca tggcctcccg ccacggggcc        360

gtgctgtgtt tatggctggc agaggcagcc agcgggtggg ggattctgct gctcgctcac        420

ctgcctggct cgctggtctc tcgaatttttc ttccctctga aatcctat                   468


<210> SEQ ID NO 260
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 260

ctgcaccaac tcatgctgga ctgttggcag aaggaccgca accaccggcc caagttcggc        60

caaattgtca acacgctaga caagatgatc cgcaatccca acagcctcaa agccatggcg        120

cccctctcct ctggcatcaa cctgccgctg ctggaccgca cgatccccga ctacaccagc        180

tttaacacgg tggacgagtg gctgaaggcc atcaagatgg ggcagtacaa ggagagcttc        240
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gccaatgccg gcttcacctc ctttgacgtc gtgtctcaga tgatgatgga ggacattctc       300

cgggttgggg tcactttggc tggccaccag aaaaaaatcc tgaacagtat ccaggtgatg       360

cgggcgcaga tgaaccagat tcagtctgtg gaggtttgac attcacctgc ctcggctcac       420

ctcttcctcc aagccccgcc ccctctgccc cacgtgccgg ccctcctggt gctctatcca       480

ctgcagggcc agccactcgc caggaggcca cgggcacggg aagaaccaag c                531


<210> SEQ ID NO 261
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (331)..(331)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 261

cctcggacac cagagacaat aactgagcgc ggaggacacg cctgccctgc ctgccatctg        60

tggcccgaag ccattgccat ccactgcaga cgcctggaga gggacaggcc gcttccgagt       120

gcagtcctgg cgcagcaccg actcccacgc acccggggaa ggacaccctc actcccacac       180

cccgggaaga acactagaac atcagcagan gggccctgcc cctccgcctg cagccgtgaa       240

aggaagctgg gtcatcagcc cagccccgcc caccccagcc cctatgtgtg tttccctcaa       300

taaggagatg ccttgttctt ttccaccatgc naataacatg cccagcaaaa acttgcttta     360

tgggtctgcc tggagaaaa                                                     379


<210> SEQ ID NO 262
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

aaccacacca gaagacatcc tcaggaacaa aggctgctcc agctctacca gtgtcctcct        60

cacccttgac aacaacgtgg tgaatggttc cagccctgcc atccgcacta actacattgg       120

ccacaagaca aaggacttgc aagccatctg cggcatctcc tgtgatgagc tgtccagcat       180

ggtcctggaa ctcaggggcc tgcgcaccat tgtgaccacg ctgcaggaca gcatccgcaa       240

agtgactgaa gagaacaaag agttggccaa tgagctgagg cggcctcccc tatgctatca       300

caacggagtt cagtacagaa ataacgagga atggactgtt gatagctgca ctgagtgtca       360

ctgtcagaac tcagttacca tctgcaaaaa ggtgtcctgc cccatcatgc cctgctccaa       420

tgccacagtt cctgatggag aatgctgtcc tcgctgttgg cccagcgact ctgcggacga       480

tggctg                                                                   486


<210> SEQ ID NO 263
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

tctccgtgga ggctatggct tcagacaggc cccgaaggtc tgtcaccaat gtgctcggtt        60

gtgggtcaca taacgctctc tggagggctt gcctttcagc ttgggatcat gaaaagatga       120

tttgacgctg tttctcatgg tctccgacct aataaagcaa gataagagaa aacaaatgtt       180
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attttaaaaa aatcaccctt tggcaaaaga aacatgtaaa attagaatct ggcacaaaca      240

aaacctgaat ctgggttgtg aactttcacc acccgccgca actctttgat aaaacctcaa      300

gtgatatcta ttaccattgt aaaaataaag cctgcccta tgcttagaat                  350


<210> SEQ ID NO 264
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

ggcaaccggg gaagtattgt ggccttggag tttgctaaat ccaaatatga aaatcaaaag       60

ctttagtatt cctcatcttc tcttctggaa gatttgcgtt agagtttttg ttgggccttc      120

aaaaagctgt gttcagagtt aggagaatat atccaataaa agatggtttc gtctaccaat      180

tggggaagtt tcaccctctc cctatctgaa gaaaaaaatc aaaaacaaat gtccccggat      240

ctttcgatgc aagtcctgga ggcagggaga tcactgcctg cctggcccac gctgctggga      300

cggctcgtcc tccctgcttt ttgttttttca aacctcctgc ttctcccacc ttgggaagga      360

gaaatgtgaa acccggcagc ggccgaccta ggcggtcttg tggcccggag ccggcccggc      420

ccgaaaacca tagacctggt tgtactgtag cttgttgttt gggggaccaa attttctaga      480

gagaactaga gcacttttgt tgtgttt                                          507


<210> SEQ ID NO 265
<211> LENGTH: 192
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 265

cacaggcctt cagaggcgat ggctgggcga cagtgacgaa agcaaagcaa agcagggctg       60

tggagacact cctcgcattt gtctcttccc tccaaggatt atctgagcaa gtcgacttgt      120

tcattcaaag gcggggtctg ccaagccctg ctctatccaa tggggatagc ttctacgtaa      180

cggattccaa tt                                                          192


<210> SEQ ID NO 266
<211> LENGTH: 202
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 266

agagcaacag ctctatatct ggatcactgc agtgcctaga agatacaaca gcacaattta       60

caaatccaaa tttccaggaa gtctctgcac atacctctag tacaaaagat gtttcagaga      120

ctagagggtc agaaggcaaa gagaggcaat attcaactcc cagttcaggt caaaagggaa      180

gaaagcctgg tgttgaaaga aa                                               202


<210> SEQ ID NO 267
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 267

gaaccacgtt ctttgtatgg gcccaatgag ctgtcaagct gccctgtgtt catttcattt       60

ggaattgccc cctctggttc ctctgtatac tactgcttca tctctaaaga cagctcatcc      120

tcctccttca cccctgaatt tccagagcac ttcatctgct ccttcatcac aagtccagtt      180
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ttctgccact agtctgaatt tcatgagaag atgccgattt ggttcctgtg ggtcctcagc      240

actattcagt acagtgcttg atgcacagca ggcactca                              278


<210> SEQ ID NO 268
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 268

ctcctggcct gatactctag ggatgcaggt gggagaagca ggggtcctgg gggctgcctg       60

gagctctggg aggcattctg aacggggtct actactgatc tcaggtgagc tctgccctcc      120

tctgaaagtc acttttctca tcagttaaat gggggcaagg gtccgtggtc cgaccaaggt      180

cttggcttca cagacatcac caggagcctg catgccctg atcactcctt ctccttcctc      240

caggaaactc cagcctggcc tctgacccca gttcaatccg accatgccca agcccaagcg      300

gnccttтcct ccagaactgc tccggggcct ggctgtgtga ctggagcaag gtgctaaacc      360

tctctgtgcc tcgctggtct aatctgtaaa at                                    392


<210> SEQ ID NO 269
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (240)..(240)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 269

taatctcatc caaaaccatg ctcacagaca cacccagcat aatgtttgac caagtatctg       60

ggcaccttgt ggttcagtca aattaacaca tattaactac cttagcaaga tgaaaagcag      120

tgaatgcagg atggtggttg aaattttaaa tacgttggtt atatagtctc attgaaaaag      180

gaacatttga gtgaagactt gaaggggtgg tggaataaac catttatttg cttattgccn      240

gtctccctct atcagaatga aagcttcatg aagcgagaga cttaattttt atctgttata      300

tccctagtgc ctggtgcagg gtaagtactc aaaaatattt gttgagtgaa taagtaatga      360

ttgaggatgg ggactggttt gtatctggtt atatctcttg tccttagcac agtacct        417


<210> SEQ ID NO 270
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 270

ggggccctag ggattatagc caggactcta atctgcctac catgccattt aacaagagat       60

cccactctcc agctgccttg tgtccctagg gtcctggcca tgtgtttagt gtgctaaact      120

ttctcctttg ttctcaggcc ttccaggtag tccccttcct ggacttaaga gtgcaaactc      180

ttctctgtgg ttctagcctt gggcagaatt atatcccaga gaccacagag caactgtcaa      240

gctgcttacc ccctcaccca gggctacagc ctgtgcccag ccctctaatt tgtgcctctc      300

ttgtgttggg ggtggtgggg gttattcctt tccctttcct gctctggcct ccttgaaagt      360

tcagagtacc cagtacaagt cagccaccat gctgacgggt attttтcctc at              412
```

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```
<210> SEQ ID NO 271
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (76)..(76)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (270)..(270)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (347)..(347)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 271

tagccaggta tagtggcagg aacctgtaat cccagctaca ggggaggctg aggcaggaga      60

atcgcttgaa cccggnaggt gtaggttgca gtgagccgag attgcaccac tgcactccag     120

cctgggcgac agagcgagac tctgtctcga aaaaaaaaa ggtccgtgcc aagctgctcc      180

ctgcccttgc cctttccctt tccctggggt ccaaaccaca tgtgtcctgc ctctcctggc     240

cctaccacat tctggtgctg tcctcactcn cccctggccc agaggctcct gaagatgctg     300

ggcggtcctg gcacagggag gagcagctct gtaaatctgt gcacatngcc actcttggcc     360

taataaagga gg                                                        372


<210> SEQ ID NO 272
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 272

cctaccaccg tcttcgagag gatgtcatgc ggctctctcg cctagcactg ggctcagagg      60

cctggcgccg agtctggagc cgcagtctgc agctggcgag ttggccaaac cggggagggg     120

cacctggagc tccccagggt gaccctatga gggtattctc agttaggacc cggagacagg     180

acactcttcc tgaagcgggg cgcagatcag aggcagaaga ggaggaggcc aggaccatca     240

gagtgacacc tgtcaggggc cgagagaggc tcaatgagga ggagcctcca ggtgggcaag     300

acccttggaa attgctgaag gagcaagagg agcggaagaa gtgtgtcatc tgccaggacc     360

agagcaagac agtgttgctc ctgccctgcc ggcatctgtg cctgtgccag gcctgcactg     420

aaatcct                                                              427


<210> SEQ ID NO 273
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 273

gtccacattc ctgcaagcat tgattgagac atttgcacaa tctaaaatgt aagcaaagta      60

gtcattaaaa atacaccctc tacttgggct ttatactgca tacaaattta ctcatgagcc     120

ttcctttgag gaaggatgtg gatctccaaa taaagattta gtgtttattt tgagctctgc     180

atcttaacaa gatgatctga acacctctcc tttgtatcaa taaatagccc tgttattctg     240

aagtgagagg accaagtata gtaaaatgct gacatctaaa actaaataaa tagaaaacac     300

caggccagaa ctatagtcat actcacacaa agggagaaat ttaaactcga accaagcaaa     360

aggcttcacg gaaatagcat ggaaaaacaa tgcttccagt ggccacttcc taaggaggaa     420
```

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```
caacccgtc tgatctcaga attggcacca cgtgagcttg ctaagtgata atatctgttt      480

ctactacgga tttaggcaac aggacctgta cattgtcaca ttgcat                    526


<210> SEQ ID NO 274
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 274

tgtgtccact ggtttcagtc tgagttctct gcactttgag gatgcagaca gtgaagttct       60

cccatggtta tagggggaga gatcatagga atgctatgga aagaggcctg aagtcagagc      120

cagctagtgg ttattattta ttaattgcct gtgaggtgcc aggcgcacat attagaccat      180

atgtgattgc agtgagccac ccggatcccc ttcaagctgc tgctgcagct gatggaagtc      240

ctattggcag acagccttct ctcatcagcc ccttcaggac ttgcctcagt tgcagagagc      300

tgccttcccc aagatcacac ccttccctgg ggactcacaa ccaatggctg atccagaaga      360

atccataaag cccgtatcat ttcagcccaa tttaggacag ctttgttgag ccattagacc      420

tacatgcag                                                             429


<210> SEQ ID NO 275
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (376)..(390)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 275

gaagctctac ttgcctggtg gtaattccag gatgacccag gagaggctgg aaagagcgtt       60

caaacggcag ggcagccagc ccgcacctgt caggaaaaat cagttgctgc cgtctgacaa      120

ggtggatggt gagctgggtg ccctgcggct cgaggatgtg gaggatgagt tgataaggga      180

agaggtcatc ctgtcgccag tcccatcagt gctcaagttg cagacagcat caaaaccaat      240

tgacctctca gtagcaaagg aaataaagac ccttctgttt ggttccagct tttgctgttt      300

caatgaagaa tggaaacttc agagtttttc ctttagtaac acagcctcat taaaatacgg      360

catagtgcag aacaannnnn nnnnnnnnnn agtcctggca gctgtccaag gctgtgtcct      420

acagaaactc ctgt                                                       434


<210> SEQ ID NO 276
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 276

aaaatcactg ccactgactt ttaccctctt caggaagagg ccaaggagga ggaacgcctc       60

atagctttga agaaaatcct cagctcgggg gtgttctatt tctcatggcc aaacgatggg      120

tctcgctttg acctgactgt ccgcacgcag aagcaggggg atgacagctc tgaatggggg      180

aactccttc                                                             189


<210> SEQ ID NO 277
<211> LENGTH: 542
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 277
```

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```
gaggagcagg caaggctacg tgggcagctg aaggagcaaa gcgtgcgctg ccggcgcctc        60

gctcacctgc tggcctcggc ccagaaggag cctgaggcag cagccccagc cccagggacc       120

gggggtgatt ctgtgtgtgg ggagaccac cgggccctgc aggggggcat ggagaagctg        180

cagagccgct ttatggagct catgcaggag aaggcagacc tgaaggagag gccagggagg       240

gttctccccg tgcaaccccc actgcacagc agatcatgca gctgcttcgt gagatgcaga       300

accccgggga gcgcccaggc ttgggcagca acccctgcat tccttttttt taccgggctg       360

acgagaatga tgaggtgaag atcactgtca tctaaaagcc ggctactgtc agcaaagcct       420

gaagaagtgg ggctggatac cctgcccca ccatatccct accatccctt ctcagtcaac        480

cctttaccct tacagtagca agcatagacc cctgtctaac gggggtagac aggtgcagat       540

ga                                                                     542
```

```
<210> SEQ ID NO 278
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 278
```

```
gacagtctac cgtcacgaga agcgggtgaa actgcagatc tgggacacag ctgggcagga        60

gcggtaccgg accatcacaa cagcctatta ccgtgggggcc atgggcttca ttctgatgta      120

tgacatcacc aatgaagagt ccttcaatgc tgtccaagac tgggctactc agatcaagac       180

ctactcctgg gacaatgcac aagttattct ggtggggaac aagtgtgaca tggaggaaga       240

gagggttgtt cccactgaga agggccagct ccttgcagag cagcttgggt ttgatttctt       300

tgaagccagt gcaaaggaga acatcagtgt aaggcaggcc tttgagcgcc tggtggatgc       360

catttgtgac aagatgtctg attcgctgga cacagacccg tcgatgctgg gctcctccaa       420

gaacacgcgt ctctcggaca ccccaccgct gctgcagcag aactgctcat gctag          475
```

```
<210> SEQ ID NO 279
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (225)..(228)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (231)..(231)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 279
```

```
tttttagat ctaccctctt gttgcccagg gggagtccag tggcgtgatc ttggctcact        60

gcaaccgccg cctcccgggt tcaagcaatt ctcctgcctc agtctcccga gtgtcttctg       120

tcttttgtaa aagttttca tgcccaagtg agattaattg tttaaaaaaa aaaaaacaag        180

aagaaaacaa catagatta ccgcaagacc tattgatata ttatnnnnca nggtggtata        240

cccagggtgg gtgtgacaca gaccaaaaga ggctgtgtgt tctgttgttg ataa            294
```

```
<210> SEQ ID NO 280
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (129)..(129)
```

```
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (136)..(137)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (146)..(146)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (323)..(323)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 280

ggaagcgtgt ctgctgggag tttgcgaccg atgactatga cattggcttt ggagtttatt        60

ttgactggac ccctgtaact agcactgaca taactgtgca ggtcagtgat tccagtgacg       120

atgaggatna agaagnnagg aagagnagga agagattgaa gaacccgttc cagctggaga       180

tgtggagaga ggctccagga gctccttgcg gggtcgctat ggggaggtca tgcctgtgta       240

ccggcgggac agccaccgag acgtgcaggc tggcagccat gactaccctg gtgagggcat       300

ctacctgctc aagttcgaca acncctactc cctgctgcgc aacaagactc tctacttcca       360

catctactac accagctgaa ggactgctgt gacaggggca ggctgtattt gctggctgaa       420

g                                                                        421


<210> SEQ ID NO 281
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 281

atgagaacgg cgtcttcatg tgcgccgagg gcaccggcaa gttctgtccc ctgaggtcct        60

tcccagacac tgtctacaag aagctggtcc agagagagaa gactttaaag gttagaggag       120

tggaccgcac tccctacctg ggggatgtcg ctgttgtcgt gcaccctggg aaaaaagaga       180

tgggaacccc actcgcagac actcctaccc ggcccgtcac ccggcatggg ggcatgaggg       240

accttcacga atccagcttc agcctctctg gctctcagat cgatgaccat gttccaaagc       300

gagcttcagc tcggatcctc gctcctcccg gaggcaggtc gagtggcatt tggtaaaggc       360

attgccaagc cccccgagtg aggacgcacc gccgccacca gcccgcaact ctccagccga       420

agctgcaggg gcaggagagg ctgggctggg tggcacacca cccgagggg gccccgggac       480

ccacggagcc ctccctatgt ctgcaaagtg attcactgtg cttcgagcca actctaacag       540

gcac                                                                     544


<210> SEQ ID NO 282
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 282

ctgattctac ttctgcaggg ttccacagaa gtctccagtc ttcaaatctt cagtgtatga        60

aagcacagat tcctgaaaga atggcctcaa atgaccagga gtaggagctc tctatatccc       120

tgctcctgaa aaacaagcta actggagtct ccatcacctg ccaccagcta tacacactac       180

caactaccca actgaactcc atgactgatt tgccagctaa tcatgcccct gacccagccc       240

acatggacat gggaaggaca tcagtgaact gtgaaaagag gcagagactc actcccgttt       300

gtattatgaa aacacacgcc aataggacat aaaaagaagc aagagtactg ggctttacca       360
```

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```
tgagttcaaa tctcatttct ggcaattcct atgtctaaaa aaagcttcgt aatctctttt      420

gagccctcac                                                             430
```

<210> SEQ ID NO 283
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 283

```
ccagaggatg atagcacctg tcagtgccag gcgtgcgggc ctcaccaagc cgcgggtcca       60

gatcttggtt cctctaatga tggctgccct cagctgttcc aggagcggtc agtcatagtg      120

gagaactcct caggctctac cagcgcttct gagctcctca aacccatgaa gaagaggaag      180

cgcagggaat accagagccc atcagaggag gagtcggag                             219
```

<210> SEQ ID NO 284
<211> LENGTH: 232
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 284

```
tttgcctgag gttgactata catacaaata ttgagcattt cctcctggtc tccgtgataa       60

acaaaggttt tgatattgtt cggcgagatg gaaagaaaat atcaaggagt gagctgaagc      120

cactgccctt gagaaccctc tcgaggagtc tggcctcatg aagatgccag aataaacggc      180

agatatatcc tgaatgaatg tgagattttt accctgtgaa tttcctgtga gg             232
```

<210> SEQ ID NO 285
<211> LENGTH: 249
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (208)..(208)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 285

```
agtgcttcca gtggcccaaa aatgcttttt gaagtgtgtt ttgaaacagc ccccaccaac       60

atacacccca ccaggagtac tgatcctgcc tcccttcatg tctaggggaa gcattcgcct      120

ttgagcactt gtttgcaaat ctggggagtt tgagacctcc tagcatctct tcccttcttt      180

ccctgcagtc tattcactcc cgcagccnaa aaatctctgg cgttcaggtt agcagtttct      240

gggttggtt                                                              249
```

<210> SEQ ID NO 286
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (138)..(140)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (142)..(143)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (371)..(371)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 286

-continued

```
gggaattacc ttttgtattg cttgaattta ctgctgtctg tatgaactct ttttcagata      60

aattttttaag aaatcagata agtgaagtga aagagagaga tcaaagtgtt gtggcagcac    120

aaaggagaga ctgactannn tnntgctggg gaatctgaaa gagtgctttg gtggaggtaa    180

catgagatca gggccttgaa gggtgagtca agtctgtcaa ggagacaaga gggagagaag    240

agcttgccag aggcccagag accagcgagg aggctgtggt gtcctggaat gagggcgaga    300

tacttggtgg gactggtcaa cacggcaatg aagagggata tggccgagga aaatggagag    360

gggcactgga nctgtgccag caaggactgg gatgcgtgga cttgatcctg tagataacgg    420

gaggaagaaa ggcctggatg cagcgccatg tcatgagcac atctgatcat gacagctcac    480

ctatgggagg attctccctc aacattttc                                      510
```

```
<210> SEQ ID NO 287
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)..(89)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (106)..(107)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (272)..(274)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

```
<400> SEQUENCE: 287
```

```
aggatgtgac agtgactcgg ggcgaccagg ctatgtttnc ttgcatcgta aacttccagc      60

tgccaaagga ggagatcacc tattcctgna agttcgcagg aggagnnctc cggactcagg    120

acttgtccta tttccgagat atgccgcggg ccgaaggata cctggcgcgg atccggccgg    180

ctcagctcac gcaccgcggg acgttctcct gcgtgatcaa gcaagaccag cgccccctgg    240

cccggctcta cttctttctt aacgtgacgg gnnngccccc gcgggcggag acagagttgc    300

aggcctcgtt ccgggaagtg ctgcgctggg cgccgcggga tgccgagctg atcgagccct    360

ggaggcccag cctgggcgag ctgctggcca ggcccgaggc tctgacgccc agcaatctgt    420

tcctgcttgc agtcctcggg gccctcgcat cagcgagtgc gacagtgttg gcgtggatgt    480

tctttcgatg gtactgcagt ggcaactaac aaaggtatct ttcctccttc cctatcctat    540

ttccatcctg aaaat                                                      555
```

```
<210> SEQ ID NO 288
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 288
```

```
atgtatccgc tgtcaactac gaatttgagg atgaatactt cagtaatacc agtgccctag      60

ccaaagattt cataagaaga cttctggtca aggatccaaa gaagagaatg acaattcaag    120

atagtttgca gcatccctgg atcaagccta aagatacaca acaggcactt agtagaaaag    180

catcagcagt aaacatggag aaaattcaaga agtttgcagc ccggaaaaaa tggaaacaat    240

ccgttcgctt gatatcactg tgccaaagat tatccaggtc attcctgtcc agaagtaaca    300
```

-continued

```
tgagtgttgc cagaagcgat gatactctgg atgaggaaga ctcctttgtg atgaaagcca    360

tcatccatgc catcaacgat g                                             381


<210> SEQ ID NO 289
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 289

cacgctcctg gaacgtcaga tcattattga ggcaaatgat cgccatctag aatcagcagg     60

acagactgag atcttccgaa agcacccccg caaagcctcc atcctcaaca tgccactagt    120

gacaacactt ttctactcct gcttctatca ctacacagag gctgagggga cattcagcag    180

tcccgtcaac ctgaagaaga catttaagat cccagataaa cagtatgtgc tgacagccct    240

ggctgctcgt gccaagcttc gagcctggaa tgatgtagat gccctattca ccacaaagaa    300

ctggctgggc tataccaaga agagagcacc cattggcttc catcgggttg tcgaaatttt    360

gcacaagaac aatgcccctg tgcagatatt acaggagtat gtcaatctgg tggaagatgt    420

ggacacgaag ttgaacttag ccactaagtt caagtgccat gatgtcgtca ttgataccta    480

ccgggacc                                                            488


<210> SEQ ID NO 290
<211> LENGTH: 306
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 290

tttcatgact tctccttcac ctaagcacct caaaacagat gatagcactt caggattgac     60

gcgaagcatc ttcaaatatt tggagagcta acaccatcaa aggtgccaaa atctacattg    120

agactgcttt gagaagtttc tagcactgaa agttggaatt gacactccag ccaatgatcc    180

ttccttcttt cataatcaat gcaataagat tgcagacaga aattccagtg atttctactg    240

cacagctctg gacatctctt ttcctagtat tattccctga attggccact gatttcaatt    300

ctgcag                                                              306


<210> SEQ ID NO 291
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 291

ctcctgggtc cgcagtgtac tgcgagggag cacagatgtc catccccgc tggggtggag       60

agcggcagca ggcctgatgg atgagggatc gtggcttccc ggcccagaga catgaggtgt    120

ccagggccag gccccccacc ctcagttggg gctgttccgg gggtgactgt gagcgatccc    180

accccaaacc tgagatgggg tagcccgtcc tgtgtcctcc acaggdacaa gcagtgggag    240

gagtctgaat ggtcaccagg aagcccgggc tccatcttga cctcctttt caggdacagg    300

agcaacaggc ccctcttccc tgactctaag cccttccctg taaggtga               348


<210> SEQ ID NO 292
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (343)..(343)
```

<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (361)..(361)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 292

```
tctctgcttt ccctcttatg aaaatggcag atgccttttt gtgaaggtct caaagcccac      60

ttcatcctgg ctgcagcacc aaaaggacaa aggcccgctt ttgaagtgcc tgataaggca     120

ttcctttcac ccctccatga ggaaggtggc aaatcttgag actccctatt agagagcttc     180

gattttcctg aaattgtgtt aggaaaatag ggtgacttgg tttgatcttg gtttctatac     240

ctattatggc tgcctgactc tggtcatttg gcccctgcag gcctaagcca cttggttttg     300

cttcacatat tggggtttat tagaacagta cgtagggaag canatgccag aggcacccgt     360

nccttttccc tgccttctag gtgctcctgg gaaat                                 395
```

<210> SEQ ID NO 293
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 293

```
accaagatct ctgcctggca caataacgtg gagaaaaccc tgccctccac caaggccacg      60

cgggtgggcg tgcttctcaa ctgtgaccac ggctttgtca tcttcttcgc tgttgccgac     120

aaggtccacc tgatgtataa gttcagggtg gactttactg aggctttgta cccggctttc     180

tgggtatttt ctgctggtgc cacactctcc atctgctccc ccaagtaggc aggctgtagg     240

cacttgggct gactgcctgc agaagtccca agaccctagt gaaaatacag caggcagaac     300

tctccttgga taattccccc aagaggtccc caaggattgg gagcatggga ggggagctgg     360

cgggagggtg ggaggtggga tttagccagg aaaggggtga gagtgattgt gttgtgggcg     420

aggaggcgtt tccacccccct ggtgcctatc agggcaggt gacctactcc ccattgttct      480

ggaaatctcc aggctgctgg gcagctgggc agctgggcag agctctggga agtgaagtca     540

tgagtgcccg attcctc                                                     557
```

<210> SEQ ID NO 294
<211> LENGTH: 547
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 294

```
ggttcgggtg agggcactct atgactacgc tggccaggaa gctgatgagc tgagcttccg      60

agcagggggag gagctgctga agatgagtga ggaggacgag cagggctggt gccaaggcca     120

gttgcagagt ggccgcattg gcctgtaccc tgccaactac gtggagtgtg tgggcgcctg     180

agtgtcctga cagcccttct gcaacgttta cccaccctgg ttcagagccc agcttctcct     240

ggagagccgg accctcaggg ccctgaaccg tcgctctctg gctgctcctc tgtcccttga     300

gggaggaagt cctgggaccc agggagggga ggggcctttg tctagggaag ggactggtag     360

ggaagggacg agtctaggct gagggcaaga tgggaggtca gaggtgacag aagcgttcag     420

gggtgcctgg gcctccccag gagctgtgga ctcagttcct gacctctgct ttggggttcc     480

tggggtgggc ttggggtgag tgtagttctg gcctagcagc accctcttgt ggcttgttct     540

agcgtgt                                                                547
```

-continued

```
<210> SEQ ID NO 295
<211> LENGTH: 147
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 295

tgtatgtgac caaaggtagg tcctgggatg acagcaatgc tgacactggc ctaaggagtt      60

actcatccat ttaataagta ttccagcaga tacagatgtg aacagtcaag tctctgccat     120

ccacaatgct tgtgttctaa tgcaaga                                        147


<210> SEQ ID NO 296
<211> LENGTH: 83
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 296

atgtgttcaa ccaagcggga aactctccgg gtagagtgaa atccgaagtt gctatgctac      60

aagataacct gggccgtgcg ccg                                             83


<210> SEQ ID NO 297
<211> LENGTH: 545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 297

gtctttctga gagtttcatt gccattatca acaagagaag ttgaaattta caagtcagga      60

ggttattttt ccagattgat aaccatagaa agtgaataaa cacttttaag gtcgcaaaca     120

tttgctaggt tgtccttctc aatgcatgtg caggctgcat cctgtccttg tttttaagcc     180

agggtttata aataagtaga tttataccaa tcttaataga attgtatatt ttatgcaaga     240

attaaatgct ttacaacatg aagtataact caacccattg taaactttgg tggcaatatg     300

gatttgaaac tcgacagttc tcttgtattt gcttcctagg tttctgcatg caagttatga     360

caggtaggac tgaaaaaaca ctgccttttg acttctagca tttagcaacc gagagtcgta     420

gagtcaataa agctgtaagt gtcttcactt aatctgtggt tctcctaaaa ctattatctg     480

aaacctacag catcccacca tgaaatattt ggtaaattta tgttgtgacg tgttgcagca     540

tgtaa                                                               545


<210> SEQ ID NO 298
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 298

aatttgtctg tgacccagat gccctcttct ccatggcttt cccggataac cagcgtccgt      60

tcctgaaggc agagtccgag tgccacctca gcgaggagga caccctgccg ctgacccact     120

ttgaagacag ccccgcttac ctcctggaca tggaccgctg cagcagcctc ccctatgccg     180

aaggctttgc ttactaagtt tctgagtggc ggagtggcca aaccctagag ctagcagttc     240

ccattcaggc aaacaagggc agtggttttg tttgtgtttt tggttgttcc taaagcttgc     300

cctttgagta ttatctggag aacccaagct gtctctggat tggcaccctt aaagacagat     360

acattggctg gggagtggga acagggaggg gcagaaaacc accaaaaggc cagtgcctca     420

actcttgatt ctgatgaggt ttctgggaag agatcaaaat ggagtctcct taccatggac     480

aatac                                                               485
```

<210> SEQ ID NO 299
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(36)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (40)..(40)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (312)..(312)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 299

acagcttagc gatggagaaa atggcatccc tgttgntntn tcaccagata aattgcctgg   60

atctctggga caccccgtc cccaggagaa ggatgtttgg gaagagatgg atgccaacaa   120

aaacaagata aagcttggaa tttgtaaggc tgctactgaa gaggagaaca gccatggcca   180

ggcaaatggt cttctcaatg ctccaagcct tgggtcacca attcgtgtcc gctcagagat   240

tactcagcca gacagagata ttccactggt gcgaaagtta cgttccattc acagctttga   300

gctggaaaaa cntctgaccc tggagccaaa gccagacact gacaagttcc ttgagacctg   360

gtataaaata gtgtattttt ctttttaaag cttctaaggt accattatt   409

<210> SEQ ID NO 300
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (150)..(150)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (164)..(164)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (170)..(170)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (173)..(174)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (185)..(185)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (187)..(187)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (207)..(207)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (220)..(220)
<223> OTHER INFORMATION: n is a, c, g, t or u

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (390)..(390)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (393)..(393)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (395)..(398)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (400)..(400)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (403)..(403)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 300

gagggccaag agctagggac agggggaaga gactggccca ggtggtaggg aggaaagaac      60

tcccagagtt tcctttagcc aggaaacctg ctctactgac cccgtgactt ggacagtcag     120

acatcaccct gagagtgaca agtgtaaaan tgactccctt cctnccccgn ccnncggaag     180

tatantnaga tacttgaaag cagtccnttn ctaaaatggn cttacctatg tggcctgaac     240

gattaaaaga aagaactcag agttacaagg gaaaaagaaa aagagttaca agggaattgt     300

agtctttttc tgaatagaat attagtactg tggtattgca tttcatggga atggaaatgt     360

attggtaaag ctacctgatg gaagctttcn ctngnnnncn aanatggagg gtgtattatg     420

tgcagttatt                                                            430


<210> SEQ ID NO 301
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(69)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(76)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(82)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (129)..(129)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (134)..(134)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (168)..(168)
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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (216)..(216)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (228)..(228)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (254)..(254)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (276)..(276)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 301

atcgaagaac aaagagtgct ccaaaaaata ggtcattctt ttattttcat aaagtatcta   60

aactgtanna anannnannn nngtgtttca ttctaaattn gcagctgaaa taaatttatt   120

ngcgatagna gaantatctt attattcatc ctcagaaata aaggattnga agggatagag   180

attatatgat aaatttatag aagactttca gaattntgaa tgcatttngt ttagtgttat   240

gaaatgacaa tagnaaaaaa gtctcgactt caattnaaaa gttacacaaa caaacaaatc   300

tacaggcatg tctttatata ccatcaggtc taagttttca aagaaatgg tagatataac   360

tgcagataac tcattacagt cataatctct gcccatgtgt attgagaggg ggcagttgtg   420

cacgaaaaaa gaatttatgt ggccatttta ataaattcag tttaaaatag acttgtgtat   480

atgcatgaat catcagagat gaaactggtt tgagagactc atgtgaacct tacgaa   536

<210> SEQ ID NO 302
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 302

ctggtacgct gctgctgcag ttaccagaaa aactcataag caaatacaac tggatcaagc   60

aatggaaact tggactgaaa tttgatggga agaatgagga cctggttgat aaaattaaag   120

agtcccttac tctgctgagg aagaaggttt ggaacctgta gtgtcctgtc tgataagggt   180

gaagctctcg ttcttgcttg ccccagaaga ccagtttta gtcttcactc agtggatttt   240

caaatgctct tggctgattt ttaggcaaaa tggtttttaaa tgaattcaaa ctcttcccac   300

gagggcttta gtaaaatggg aagtaccaac attatatatt cttagagcag atgccatgta   360

ctagggtatc a   371

<210> SEQ ID NO 303
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (223)..(223)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (227)..(227)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 303

gaagctgtgt ggagtggaag atggacattg aggaagaagg gcaggtgtgg tctcacccag   60

aatggttcct gctgcttccg cggtgcccag gctttctca cggcctctgc tgggttctcc   120

cctgggtgct gtggatgcat cctgcctgct ggaaattctg tgctctctgt ttccatccct   180

ttgtcgtggt aatgaccgta tacctctccc ctgtaccctc ctntgcntgc tctccgtgca   240

ggcccctctc cctctggttg tcccatcagc atttccccac agctcgttgt tcctccttcc   300

tcttttctgg tgacctttct actgattgca ttgtacctct ttccctgata ttaaa   355

<210> SEQ ID NO 304
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

gcctgtgtct tcgggctgaa tttgatctgg ccatcccagg gggtctcctc cctgagtgcc   60

cttgtgcccc tgaacatgtt cactgaactg ctgatcgagt actatgaaaa gatcttcagc   120

accccggagg cacctgggga gcacggcctg gcaccatggg aacaggggag cagggcagcc   180

cctttgcagg aggctgtgcc acggacacaa gccacgggcc tcaccaagcc taccctacct   240

ccgagtcccc tgatggcagc cagaagacgt ctctagtgtt gcgaacactc tgtatgtttc   300

gagctacctc ccacacctgt ctgtgcactt gtatgttttg taaacttggc atctgtaaaa   360

at   362

<210> SEQ ID NO 305
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

cgaagagcaa gacccactct gttccagaag ccctataagc tggaggtgga caactcgatg   60

taaatttcat gggaaaaccc ttgtacctga catgtgagcc actcagaact caccaaaatg   120

ttcgacacca taacaacagc tactcaaact gtaaaccagg ataagaagtt gatgacttca   180

cactgtggac agttttttcca aagatgtcag aacaagactc cccatcatga taaggctccc   240

acccctctta actgtccttg ctcatgcctg cctctttcac ttggcaggat aatgcagtca   300

ttagaatttc acatgtagta gcttctgagg gtaacaacag agtgtcagat atgtcatctc   360

aacctcaaac ttttacgtaa catctcaggg gaaatgtggc tctctccatc ttgcatacag   420

ggctcccaat agaaatgaac acagagatat tgcctgtgtg tttgcagaga agatggtttc   480

tataaagagt aggaaagctg aaattatagt agagtctcct ttaaatgcac att   533

<210> SEQ ID NO 306
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (131)..(131)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (205)..(205)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 306

ggaaccctcc tcttggcaag ggctttccga agttaacctg aaaaactggt tcaggccatg   60

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```
acagcaaagg gttggatagc ctcattatcc ctcctccctt cagaactctg gaacagccag          120

cgttaacatc nacacaggcc ttcagtctga tgagaaacat ttaccatcta ttgtctcgga          180

agcctgctac ntggaggctt catcntgatg ataaagcctt ggtctccaca accccgtata          240

acccagacat tcctttctat tgataactct tgcaagcgat tgccaaccag aagatgttta          300

aatccaccta taacctggaa gcccccagtt ccagctgccc acctttctgg actaaaccaa          360

tgtatatctt caatatattt gattgatgtc tcatgtctcc ctaaaatggg taccatcaag          420

ctgtgcactg acca                                                            434
```

```
<210> SEQ ID NO 307
<211> LENGTH: 157
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 307

cctccgcaca ctggatgaga atccatcttc cattcgagct gggaatagac tttgtgaaag           60

atattatgta atggagtctc gggaaccctg agacctctcc agcgaagctg aagtgaatta          120

attaagtgct ttaaacggtc ttggtgctgt gttacgg                                   157
```

```
<210> SEQ ID NO 308
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (35)..(35)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(40)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(47)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (52)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (62)..(64)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(68)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (71)..(71)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (75)..(75)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (79)..(79)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(86)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)..(91)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (289)..(289)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 308

aggtgatgca ctatgcccag tacgtcctcc tggcnctnnn ctnnnnngcg tnncctgntn        60

cnnntcnntg ncntntgcna antnnngann nanaaccgtg taaaaccatt tttatgtggc       120

ttcaacgtca actataaatt agcttggtta tcttctagga gaaatgctat ttattttgga       180

gtagtagtaa aaagggctca aaggataagg aggccattca ggcctattct gaatccctga       240

tgacatcagc tcccaagggc tctgtgctgc aggaagcaaa actgtaggng ggtaccaggt       300

aatgccgtgc gcctccccgc cccctcccat atcaagtaga atgctggcgg cttacagact       360

gaagatg                                                                 367


<210> SEQ ID NO 309
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 309

accccaccac gtaccagatg gatgtgaacc ccgagggcaa atacagcttt ggtgccacct        60

gcgtgaagaa gtgtccccgt aattatgtgg tgacagatca cggctcgtgc gtccgagcct       120

gtggggccga cagctatgag atggaggaag acggcgtccg caagtgtaag aagtgcgaag       180

ggccttgccg caaagtgtgt aacggaatag gtattggtga atttaaagac tcactctcca       240

taaatgctac gaatattaaa cacttcaaaa actgcacctc catcagtggc gatctccaca       300

tcctgccggt ggcatttagg ggtgactcct tcacacatac tccccctctg gatccacagg       360

aactggatat tctgaaaacc gtaaaggaaa tcacaggttt gagctgaatt atcacatgaa       420

tataaatggg aaatcagtgt tttagagaga gaacttttcg acatatttcc tgttcccttg       480

gaat                                                                    484


<210> SEQ ID NO 310
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 310

ccatggggcc atctgggcca ttcagagact ggagtgagat ttgggtgtgg aggggaggc        60

gccaaggtgg aggagcttcc cactccagga ctgttgatga aagggacaga ttgaggagga       120

agtgggctct gaggctgcag ggctggaagt ccttgcccac ttcccactct cctgccccaa       180
```

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```
tctatctagt acttcccagg caaataggcc cctttgaggc tcctgagtgc cctcagatgg      240

tcaaaaccca gttttccctc tgggagccta aaccaggctg catcggaggc caggacccgg      300

atcattcact gtgataccct gccctccaga gggtgcgctc agagacacgg gcaagcatgc      360

ctcttccctt ccctggagag aaagtgtgtg atttctctcc cacctccttc cccccaccag      420

acctttgctg ggcctaaagg tcttggccat ggggacgccc tcagtctagg gatctggcca      480

cagactccct cctgtgaacc aacacagaca cccaagcaga gcaatc                     526
```

<210> SEQ ID NO 311
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 311

```
taaattgcct ggatctctgg dacacccccg tccccaggag aaggatgttt gggaagagat       60

ggatgccaac aaaaacaaga taaagcttgg aatttgtaag gctgctactg aagaggagaa      120

cagccatggc caggcaaatg gtcttctcaa tgctccaagc cttgggtcac caattcgtgt      180

ccgctcagag attactcagc cagacagaga tattccactg gtgcgaaagt tacgttccat      240

tcacagcttt gagctggaaa aacntctgac cctggagcca aagccagaca ctgacaagtt      300

ccttgagacc tggtataaa                                                   319
```

<210> SEQ ID NO 312
<211> LENGTH: 234
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(87)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)..(90)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (94)..(95)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (186)..(186)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 312

```
gcgcttgcgc agtagctgaa cgcgggcgtt tctttcctcc cttttttttcg aattggtttt      60

gggggtagat tcgagttaca aaatnnncnn cngnngngtg ttcggcgcgg ttcccccagc      120

tgtctctggc tgaaccggcg ctctcgcctc cctgccgaac acagcgtgag gagccccccc      180

agggananatgg tgtttgagtc tctgggcttg ccgagcacta agtcctctga gttc          234
```

<210> SEQ ID NO 313
<211> LENGTH: 125

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313

gtactgcaaa aatcaccctc ggcaagacga atgtctgacg tgccggaagg agtcatacgg          60

gtccatgctc cacttctctc caaggtgtcc atggccattc aactcaacaa tcaaaccaaa         120

gccaa                                                                     125


<210> SEQ ID NO 314
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (130)..(130)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (205)..(205)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (211)..(211)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 314

aagtcattcg tttaagcgtg gattattttg ccgaatgaat aatgatgatg gcngctttca          60

tctcttatga agttttcctg gccaagagcc agnagttgga agtttggatc attctttttt         120

ctttttttaan catttcttct cttctttctc ttttttatca ctaaatgaat gacatgtgga        180

gaaactattc agctttttaaa gtatnctcca nttacttgtc tcaactacca ctatttattg        240

tgtttatcaa aatcataaaa agctcatttt tggcatttac cttcgtggtt gagactgctg         300

tctgtatgtc tgggaatgga agtcctcttc agggattcag caagggctgt acttttgctt         360

aatactagtg gttccttatt ctaagtgatg acatcatcca cctttcctag aaatgggtct         420

ttgtgcctag tatgatatct ttccaa                                             446


<210> SEQ ID NO 315
<211> LENGTH: 473
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (207)..(207)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (375)..(375)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (395)..(395)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (405)..(405)
```

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<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 315

```
tgtttcaggc ccatccacag ttgaagcagt gtgtgcgtca ggcaattgaa cgggctgtcc      60

aggagctggt ccatcctgtg gtggatcgat caattaagat tgccatgact acttgtgagc     120

aaatagtcag gaaggatttt gccctggatt cggaggaatc tcgaatgcga atagcagctc     180

atcacatgat gcgtaacttg acagctngga atggctatga ttacatgcag ggaacctttg     240

ctcatgagca tatctaccaa cttnaaaaaa cagttttgcc tcagcccttc gtgtaagttg     300

gctatttcct tggtataggt acaaaacgta ttactgcttg tctgtaataa ttttttttctt     360

tgtctatata tggcnctggg cgttaccact tattnttaat aatcnccata tttgtttgat     420

gtcttccatc attttagatt gtaattctgt gaggcaaagc atcatgtctg tgt            473
```

<210> SEQ ID NO 316
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (351)..(352)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (395)..(395)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (496)..(496)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 316

```
aggacaccag gctggtggcc acagtgctgc tgtccgtggt cgtgctgctc cacgccctcc      60

tgnccatggg ctgtaagttg tacttcttcc agtcgctgcc tccggagaac gtggctcctc     120

cacccccaaat cacatctctg ccctcaaaca tcgcgctgtc ccctaccttg ccgcagtccc     180

tggccccctc ctaggaaggc ccgggtccca caggcaacac ctaagtggac caacccctct     240

gcctgtcctg ccccccagac gatgactgaa ggctcctttg acaccttgag atgattctgc     300

tactttccag acttttctta caaagcaaac acttttattt tctatgcaaa nntgattcag     360

agaatttata taaaggcggg cgaggggcag ccgancaggg agctttggga cagggctggg     420

gcccccatat cccccccggg ccacctgctt ccctcctat ggctcccctg gaacaggagg     480

gagagccaag ggggcngccc agcctggaca gcgcccgctc ctgcctgggt gcacacacgg     540

cgggcctgag ctccagcatc tgagtttggg ggtatg                              576
```

<210> SEQ ID NO 317
<211> LENGTH: 265
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 317

```
ccaggagcag ctgcgtgacg tcatgttcta cctggagaca cagcagaaga tcaaccatct      60

gcctgccgag acccggcaga aatccaggag ggacagatca acatcgccat ggcctcggcc     120

tcgagccctg cctcttcggg gggcagtggg aagttgccct ccaggaaggg ccgcagcaag     180

aggggcaagt gaccttcaga gcaacagaca tccctgagac tgttctccct gacactgtga     240
```

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gagtgtgctg ggaccttcag ctaaa   265

<210> SEQ ID NO 318
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (115)..(115)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (241)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 318

atacgtgggt agtgttgcat ttcaaatgag gctcttctgg ttgaaatgat atatttataa   60

gaccagaata tcacaaatgg gtgatgtata atgtctcttt agttttttngg tattnggcct   120

cttttaaagc ctgtcggatg tatgggagaa aacaatgaac gtgctttgat ttcctatcag   180

tcactcttaa gaacatacat atngtttaag taactcggtc ttttttatct gattcttgag   240

ncactatggg tagcaagtaa ccacttacaa atttaaatgt aatatacact ccttttctgt   300

gtgtcaagtc cttattttta ggtgcatatt gacatttaaa tgttaattat tgtttggcat   360

ataatatcaa aaatctatta tttattttat gctgttacag ttaaaagatg tgatttatga   420

catactgaat caacttgcct tccaatttag tgtgtaatat ggtaagcatt tatactttta   480

gatatgtctt atttttattt ggatgcctgt ctacc   515

<210> SEQ ID NO 319
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (147)..(147)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (159)..(159)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (161)..(161)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (167)..(167)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (172)..(172)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (181)..(181)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (188)..(188)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (220)..(220)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (260)..(260)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (509)..(509)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 319

gagttaatgc agcactcgtc attcagaaat attggcgaag agtcttagca cagagaaaat   60

tattaatgtt aaaaaaggaa aagctggaaa aagttcaaaa taaagcagca tcacttattc   120

agggatattg gagaanatat nccactngac aaagatttnc ngaaatngaa anattattca   180

ntcatccngc naatntagga taagaatgat aattgctgtn acatcttata aacgatatct   240

ttgggctaca gttacaattn cagaggcatt ggcgtgctta tttaagaaga aaacaagatc   300

aacaaagata tgaaatgcta aaatcatcaa ctcttataat ccaatctatg ttcagaaaat   360

ggaagcaacg taaaatgcaa tcacaagtaa aagctacagt aatattgcaa agagctttta   420

gagaatggca tttaagaaaa caagctaaag aagaaaattc tgctattatc atacaatcat   480

ggtatagaat gcataaagaa ttacggaant atatttatat tagatcttgt gttgttatca   540

t   541

<210> SEQ ID NO 320
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (144)..(145)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 320

cttcggattt ttattgactc aaaatagtgc cattcccctt aatgaaatag attttgagtc   60

tttttttcat tgtaacccc aaatgagaat catctacctg attcttgtac caaaaaaaaa   120

ttttttttcag tctttttttt tttnnagaga gggtctcttg tcaacgcaag actgggagtg   180

gcagtggcac gatcttagct cactacaact tctggcctcc caggctcaag caattctcct   240

gcctcagcct cctgagtagc tggggattac aggcatgcac caccacgccc agctaatttt   300

ggtattttta gtagagacag ggtttcacca ttgtttggcc aggctggtcc cgaactcctg   360

acctcaggtg atccacccac ctcggcctcc caaagtgctg ggattatagg tgcgagccat   420

tgcgcccagc ctcagttatt ttatttaaca gtgtaagtac ttagaaagta agaaaatggc   480

gtgattagtt ttttg   495

```
<210> SEQ ID NO 321
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 321

ggctgaggag gctggtctga acatcactca catttgcctc cctccagata gcagtgaagc      60

cgagattata gatgaaatct taaagatcaa tgaagatacc agagtacatg gccttgccct     120

tcagatctct gagaacttgt ttagcaacaa agtcctcaat gccttgaaac cagaaaaaga     180

tgtggatgga gtaacagaca taaacctggg gaagctggtg cgaggggatg cccatgaatg     240

ttttgtttca cctgttgcca aagctgtaat tgaacttctt gaaaaatcag taggtgtcaa     300

cctagatgga aagaagattt tggtagtggg ggcccatggg tctttggaag ctgctctaca     360

atgcctgttc cagagaaaag ggtccatgac aatgagcatc cagtggaaaa cacgccagct     420

tcaaagcaa                                                             429


<210> SEQ ID NO 322
<211> LENGTH: 467
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

tctgagggtg ccttgatgct ggctcatcac acattgagta tcttgggcat tatcatggcc      60

cttgtgcttg gggagtctgg cacagaggtc aatgcagtcc tctttggaag tgagcttacc     120

aaccccttgc tacagatgcg ctggtttctc cgggaaacag ggcactatca cagtttcact     180

ggagatgtag tggacttcct ctttgtggct ctgttcacag gagtgaggat tggtgtggga     240

gcttgcctcc ttttctgtga aatggtctcc cccacgccta agtggtttgt gaaggctggg     300

ggagtagcga tgtatgctgt gtcttggtgt ttcatgttta gcatctggcg ctttgcatgg     360

aggaagagca tcaagaagta ccatgcttgg agaagcaggc ggagtgagga acggcagctg     420

aaacacaacg gacatctcaa aatacactag ccaaggcttg ctccaga                   467


<210> SEQ ID NO 323
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

ttggcacttc agaagtctcc ccaatcttga caaagccctg agaaagggc cgggcctccc        60

gttgataaga atatcactgc agataaatgg aggtttcaaa ttgaaagaaa ggaggagggc     120

ctcctgttga taagattatt gtcactgcag gtaaatggag gcttcaaata gaaatacatt     180

tcagttacag aaaaaaaaat tatctttgtt acacatttga gtttgcaggc ctaaggttac     240

tcccgctaca ctatcatctg taaccataac gcactcaaca tttttaagcta actataagga     300

ttgttgcttc actcaaagat cctgaggttt tattcactaa catttttatt tggtgactat     360

agttgacaag aacaaagctg tggggaacca acaaacactg caatgcctgg cattgtcacc     420

tcactagatt gtgagttcct ctgggacagg gtccgtacat tttcttagaa tccctcactt     480

agccattagc ctgcacagtg cttg                                            504


<210> SEQ ID NO 324
<211> LENGTH: 163
<212> TYPE: DNA
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```
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

catggaggag tgcatttcct tggctattcc agaagtccta cctcccttct gagattttat        60

aatggtattt cttatggtta tcccaaatat acttggcaag tcgtcttata aaccaccaat       120

aatagcctct taaaaattca aaaattactc ctcttggcta aca                         163


<210> SEQ ID NO 325
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

cctccgcgga aggcgtggca gggaggcagt cgccctgcgg tgcaagctgc tgctccagag        60

cataccgtgg cccaggtggt atccccaagg cctcgtgccg tggctggggt cctgggaggt       120

ggtcgccctg cagtgcaagc tgctgctcca gagcgtaccg tggcccagac tgatcctcga       180

ggcctcctgc cgtggctggg gtcatggtcg gctgcgcatg tccagaagca tttccttcct       240

gcgaccatcc cggcgcccct aggggagaa gccaggacag cagcttccgc tgtctccaca        300

gcagacacgg gacggattcc acagacggga gcctcattcg taccatgcca aacgcattca       360

ctcggggcag tattaaccgt tctagaaagc cactgtttta tagcaaaaca ggaaaggaaa       420

agctaccagt tttttattca g                                                 441


<210> SEQ ID NO 326
<211> LENGTH: 457
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

tttcccctag ttgacctgtc tataagagaa ttatatattt ctaactatat aaccctagga        60

atttagacaa cctgaaattt attcacatat atcaaagtga gaaaatgcct caattcacat       120

agatttcttc tctttagtat aattgaccta ctttggtagt ggaatagtga atacttacta       180

taatttgact tgaatatgta gctcatcctt tacaccaact cctaatttta aataatttct       240

actctgtctt aaatgagaag tacttggttt tttttttctt aaatatgtat atgacattta       300

aatgtaactt attatttttt ttgagaccga gtcttgctct gttacccagg ctggagtgca       360

gtgggtgatc ttggctcact gcaagctctg ccctccccgg gttcgcacca ttctcctgcc       420

tcagcctccc aattagcttg gcctacagtc atctgcc                               457


<210> SEQ ID NO 327
<211> LENGTH: 438
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(96)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (218)..(218)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 327

ttgtcctttta tgtatcttct ttccatagtg cttactggag ccttccaaaa taatgtctcc   60

tcaangtgac agcccctcag gaatttgaag gcaatngtca caccctcacc cnctttcctg   120

agtttttct ggtttattaa cgtcagtctt tacagtcagt gctcattgac ggtggttttc   180

tctggttgtt tcctgaacac gtagtgctct taaagcantg ccctgaggng aatacaattc   240

tccaggggca ttctgattgg caggtgaagc acagtgccat gttcccagca ctgatttggg   300

aagtggcttg tcacatccca cagtgaactc agtcaactgg aatgcctaac tctctttcat   360

aagacctcct gctacattat gtttctccca gactgtactc aggtccaaga acagaattta   420

ctagtctatc cttctcaa   438

<210> SEQ ID NO 328
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (40)..(40)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 328

cccttcttgc tgccacagga tgaataaagt gttgagattn gtctatggag aaagctgtgt   60

gtctgttttt atctccctc tcaggaccag tcagccactg gtcaatcagg ctgatcatgg   120

aacattagga attctccaat taagggagaa aaagtccagg gacttagtta tatcttcaga   180

ccagtgcagc tgggacacac aaagttctcc tgtctcacca tctgatatgg tttggatgct   240

cgtcccctcc aaatctcatg ttgaaatgta attcccagtg ttggaagtgg agcctggtgg   300

gaagtatttg gatcatgaga gaggatcctt catgaatggc tcagcaccat ctccttggtg   360

atgagtgagt tctcactcaa ttcacataga tatggttgtt taaaagagtc tgagacctct   420

cccctctttc tcgccatgtg atatgcctgc tccccttca ccttccgcct ttactgtaag   480

cttcctgagg ccctcaccag aagctgagca aatgttggtg ccatgccagt acagc   535

<210> SEQ ID NO 329
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 329

gccacagact gaactcgcag ggagtgcagc aggaaggaac aaagacaggc aaacggcaac   60

gtagcctggg ctcactgtgc tggggcatgg cgggatcctc cacagagagg aggggaccaa   120

ttctggacag acagatgttg ggaggataca gaggagatgc cacttctcac tcaccactac   180

cagccagcct ccagaaggcc ccagagagac cctgcaagac cacggaggga gccgacactt   240

gaatgtagta ataggcaggg ggccctgcca ccccatccag ccagacccca gctgaaccat   300

gcgtcagggg cctagaggtg gagttcttag ctatccttgg ctttctgtgc cagcctggct   360

ctgcccctcc cccatgggct gtgtcctaag gcccatttga gaagctgagg ctagttccaa   420

aaacctctcc tg   432

<210> SEQ ID NO 330

-continued

```
<211> LENGTH: 234
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

agcaaatcta gctttcagta ttcctaattt ttacctaagc tcattgctcc aggctttgat      60

tacctaaaat aagcttggat aaaattgaac caacttcaag aatgcagcac ttcttaatct     120

ttagctcttt cttgggagaa gctagacttt attcattata ttgctatgac aacttcactc     180

tttcataata tataggataa attgtttaca tgattggacc ctcagattct gtta           234


<210> SEQ ID NO 331
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

acttaggagt ggtgcttttt ctcagaaaac aggccacggt gtttcataca gaatgtcttc      60

atatcatctg aaatggtatg gctgaagttc atttgtttac agggtcggga atgtcttcag     120

ttcttgagag tcaacagtaa tgattggttg taagccaagg gacattttaa gctagtgaag     180

agttttttct ggaattgatt tttcccaaaa gaatatatta attgaggtta agaagtcagt     240

gggaaacaca cagaaatttg tttttaaaatc tttcaggagc tttactgaaa gacttggtta     300

tcaagtcttt tggggag                                                     317


<210> SEQ ID NO 332
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

gacttacttt aacaaccagc caatccctac ctaagcctag tagccatggt ttggctaaga      60

ccgcagcgac tgtatttagt aaatcctttg aacaagtcag tggtgtcaca gtcccacata     120

acccgtcatc tgctgttggt tgtggggctg ggacagatgc caataggttt tccgcttgta     180

gtctccaaga agaaaagctt atttacgttt cagaaagaac tgaacttcca atgaagcatc     240

aatcaggtca gcagagacct cctagtatta gcattactct gtccacagat taattagtaa     300

catatttttc tcccataacc tagtgaacct ggaaatacaa ctttgcttct ttatgaaagt     360

accctgggtc tttcatccgt attcctgaca ggagccctga tgtcttaaat tctga          415


<210> SEQ ID NO 333
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 333

gacgggtcca ttaacaaagc gggctttgcc gtcaactttt tcaaagaggt ggacgagtgc      60

tctcggccca accgcggggg ctgtgagcag cggtgcctca cacccctggg cagctacaag     120

tgcagctgtg accccgggta cgagctggcc ccagacaagc gccgctgtga ggctgcttgt     180

ggcggattcc tcaccaagct caacggctcc atcaccagcc cgggctggcc caaggagtac     240

cccccaaca agaactgcat ctggcagctg gtggccccca cccagtaccg catctccctg     300

cagtttgact tctttgagac agagggcaat gatgtgtgca agtacgactt cgtggaggtg     360

cgcagtggac tcacagctga ctccaagctg catggcaagt ctgtggttc tgagaagccc     420

gaggtcatca cctcccagta caacaacatg cgcgtggagt tcaagtccga caacaccgtg     480
```

-continued

```
tccaaaaag                                                                    489


<210> SEQ ID NO 334
<211> LENGTH: 239
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 334

cacagataga acctgcacat tgcccattaa tgcacacttg tgtatgccta ttacagtctg      60

tgaagtttgg tttagggtca gatgctgggc agagagctgt gaagccatta catattcctt     120

cccttgcaca gtctgaatca tcccgacact tctcagactt tgacttgaat gcacactgtg     180

ctgtacaaca aggaccttga cttggactgc actgtttccc aggtttcagt ttgcatttt      239


<210> SEQ ID NO 335
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

gccctgactg actgtattct ctggccacat tcaagtcccc cattggtggg ggcagagaag      60

taggaccagg ccatccttgg ctacagagct cgaagacccc aagacagccc tctgctctca     120

gcggcgccac agagagcctg ggctcagcct tctgcatcag gacatggcct cgtccactga     180

gggcacgatt taaacatttg acatcagaag ctttatttgt aaacctcaca cagataagga     240

ccaagggctg gcggtgtggc cagaggacag gggaagctga aggccccgtg cttgagctcg     300

gcagtcctgc tccttgcagt gaagccacca tgggtgaccg tccagcctca cccggtggcc     360

tgcacagtga gggaagggct tcagggccat ctgctcccag ggcaggggac aggccaccaa     420

ggacctttgg ca                                                          432


<210> SEQ ID NO 336
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

aatgttgaca tatttcctct atctcataga tggtaaaagt gttgctttta aactggcaaa      60

tgcactcttc agaaatcctt ttctatctga tccacatgga gaggttaaag gttcaatttc     120

atgacctcta tgcaggcagc gctctcattg gatgtaagaa tattacctgc aaggatagaa     180

tgcagttgtg caacagagac acattcttat ttcttttttt tcacaatttt gttttgtttt     240

taatgaccct tttattgaat attggactga aatataaatt ttaaaaaaca cgttggaaag     300

gatgtacaac agaaggctat gtatgtatat acagtatgtc aaaagccttt tattttata      360

cttcaaatgc tctaaattaa                                                  380


<210> SEQ ID NO 337
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 337

gagtctctgc ttgataagtg cctctatacc aaccgctctc ctcatcctga catcttgata      60

cggacttctg gagaagtgcg gctgagtgac ttcttgctat ggcagacctc tcactcctgc     120

ctggtgttcc aacccgttct gtggccagag tatacatttt ggaacctctt cgaggccatc     180
```

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```
ctgcagttcc agatgaacca tagcgtgctt cagaaggccc gagacatgta tgcagaggag      240

cggaagaggc agcagctgga gagggaccag gctacagtga cagagcagct gctgcgagag      300

gggctccaag ccagtgggga cgcccagctc cgaaggacac gcttgcacaa actctcggcc      360

agacgggaag agcgagtcca aggcttcctg caggccttgg aactcaagcg agctgactgg      420

ctggcccgtc tgggcactgc atcagcctga atgaggctgg ccacctgcca ctttgccctg      480

ccctctgcct ccagggctcc actccccttc cttttcttgg tgaaaggcac ctcctttcct      540

gata                                                                     544


<210> SEQ ID NO 338
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

tcaaagaacg cgtactgcag accccaaatg accttctggc tgctggcttt gaggagcaca       60

agttcagaaa cttcttcaat gctttttaca gtgtggtgga actggtagag aaggacggct      120

cagtgtccag cctgctgaag gtgttcaacg accagagtgc ctcggaccac atcgtgcagt      180

tcctgcgcct gctcacgtcg gccttcatca ggaaccgagc agacttcttc cggcacttca      240

ttgatgagga gatggacatc aaagacttct gcactcacga agtagagccc atggccacgg      300

agtgtgacca catccagatc acggcgttgt cgcaggccct gagcattgcc ctgcaagtgg      360

agtacgtgga cgagatggat accgccctga accaccacgt gttccctgag gccgccaccc      420

cttccgttta cctgctctat aaaacatccc actacaacat cctttatgca gccgataaac      480

attgattaat tttaggccat gcagtggaac ctgtcaccta atgggactgc                  530


<210> SEQ ID NO 339
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

agtcatgcga ccaggtgagg gtccacgtcc ccaagcttcc actccctctg gtgtttccca       60

tttaagtata ctgtt                                                         75


<210> SEQ ID NO 340
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

gatgctcacg tcacttggtg taggtttcag gatcgcctct ttgaggaagg acttcaggac       60

caactggggc ctgcataaga aaacttatct cattattaga gtactcacag cttgtatctc      120

ccagctacat cctagaaccc cattgtcctt tattccacca aaccagctcc aggtgaccag      180

actctactca gaaagcaaat tcgtcatcaa agaacagaga ctggccacca caaggacatg      240

caggagaact gtcgggacca ggaagactca ttccaaaaag cccaggccgg gcacagtcgt      300

caagcctgta atcccaacac tttggggac cgaggtgggg gtatcgattg agcctcggag       360

gtcgagatca gcctgg                                                        376


<210> SEQ ID NO 341
<211> LENGTH: 499
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

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<400> SEQUENCE: 341

```
ccccgcctgt ggcattttct atgggctcag gttacacctt cccagctggt gtttctgtcc      60

caggaacctt tcttcagcct acagctcact ctccagcagg aaaccaggtg caagctggga     120

aacagtccca cattccttac agccagcaac ggccctctgg accagggcca atgaaccagg     180

gacctcaaca atcacagcca ccttcccagc aacccctttac atctttacca gctcagccaa     240

cagcacagtc tacaagccag ctgcaggttc aagctctaac tcagcaacaa caatcccta      300

caaaagctgt gccggctttg gggaaaagcc cgcctcacca ctctggattc cagcagtatc     360

aacaggcaga tgcctccaaa cagctgtgga atcccctca ggttcaaggc ccattaggga      420

aaattatgcc tgtgaaacag ccctactacc ttcagaccca agaccccata aaactgtttg     480

agccgtcatt gcaacctcc                                                   499
```

<210> SEQ ID NO 342
<211> LENGTH: 183
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (75)..(75)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 342

```
cacccgagac tgacacactg aactccactt cctcctctta aatttatttc tacttaatag      60

ccactcgtct ctttntttcc ccatctcatt gctccaagaa ttttttttctt cttactcgcc     120

aaagtcaggg ttccctctgc ccgtcccgta ttaatatttc cacttttgga actactggcc     180

ttt                                                                   183
```

<210> SEQ ID NO 343
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (239)..(242)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (400)..(400)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (405)..(409)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (411)..(416)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 343

```
tgggccttcc cttaaacatc agaacaatga gatttgtccc tattttacag gggttagaat      60

agactattaa gngacaactg agaaaggaca gagaagtgac agccagaggt tgagagggggc     120

cataaaaaca tacaatcaga catatatctg ctaccacttt gtagcaagat ggttcctatc     180

ataactctgg gtcaaaaaga tagtaatttg gtttataatg ttgaaagaaa gcagaaagnn     240

nnagatgggg tctcactgtc gttctggagt gtagtggttc aatcatctct cactgcagcc     300
```

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ttgaacccct aggctcaaag gatcctccca cctcagcctc ctgaatagct gggactagag   360

gcatgagcca ctatgtcttg ctgattaaaa attgtttttn caaannnnna nnnnnnactt   420

tactgcctaa gctggtcttg aaatcctggc ttcaagcaat cctttcactt tggcctccca   480

aaatgctggg attacaggca tgagtcaata tgcccagtct cttttctttc ttagttactc   540

tagaaaatgg cttgttga   558

<210> SEQ ID NO 344
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

aataatgttc tgtcacgtga aatatttaag tatatagtat atttatactc tagaacatgc   60

acatttatat atatatgtat atgtatatat atatagtaac tacttttat actccataca   120

taacttgata tagaaagctg tttatttatt cactgtaagt ttatttttc tacacagtaa   180

aaacttgtac tatgttaata acttgtccta tgtcaatttg tatatcatga aacacttctc   240

atcatattgt atgtaagtaa ttgcatttct gctcttccaa agctcctgcg tctgtttta   300

aagagcatgg aaaaatactg cctagaaaat gcaaatgaa ataagagaga gtagtttttc   360

agctagtttg aaggaggacg gttaacttgt atattccacc attcacattt gatgtacatg   420

tgtagggaaa gttaaaagtg ttgattacat aatcaaagct acctgtggtg atgttgccac   480

ctgttaaaat gtacactgga tatgttgtta aacacgtgtc gataat   526

<210> SEQ ID NO 345
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (334)..(334)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 345

ttgtgtacac ataatctcat tttgagatat ataactattt ttgtctttca gaagtgaatc   60

aaaatatttc aaaatgctgt cttatgaaac tacaatattc tcacagatta gaaaagtttt   120

tctgtaaaag tcagatagta aatattttag gttttgcagt gtcttttgca actactcaac   180

tttcctactg tagcacaaga gtagctgtgg tactgtgcaa ataaattgct tgtgttccaa   240

taaagcttca tttacaaaaa catgccatgg gccatatttg gcctgtacac tgttgtttgc   300

caagtcctaa tatagttgct tagcaagtat tgtnagctat ttgaggaaga catgaaagtt   360

cattgggttg ctaaaaagta tgtagaaatt caaaggaaaa ttaaaattta ggctaagtta   420

taatacactg tttta   435

<210> SEQ ID NO 346
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (95)..(95)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (227)..(227)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 346

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```
tctcatttac cttctctctt gagcaacgtc agtaattgat cttgcatctc agagagagag      60

aaagagcatg tgtgagagag aaactggttt ctatngccag cactcctgaa accccttact     120

gtaaggatat tttctcttac cccttgggat ccaggctctg agtctcttct ctttgggagt     180

atccatcaaa atgacttttt ttaaaaacag attttccccc aaccagnaga atctgcacaa     240

acttggcagc gtttttactt gtttaatgag tttaagacat tacatggtga aagagaagca     300

ttttggactc ctgcattttt atttaccatt cccagactga cga                       343
```


<210> SEQ ID NO 347
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 347

```
gcctaacaat caaatctctt tcttttaaag cacnaccttc taggcaggga caggagctca      60

ttttccacac catnctttgt caactctcat agaaagtttt ccttgtatcg agctcaaatc     120

tgcctcctgg aaattcttct tcttcttccc tccctgttgg taccagctct gctgtcagag     180

acttcacagt ctgtgctccc tctgccctgt gacgtcttca gactatttga gaacaggaat     240

catgactcct gggacttgcc ttttctctag gtcaaatacc tctataattc catctgctgt     300

tcttcatagg gtcttctccc tatcctgccc ttttcctcca atccatcttt taactgctct     360

tgagcagtct aactgagaag tatgattcaa agcaaaataa atcttaaggt ggcatgactc     420

tgaaaaaatt gagaaaattg aactcagaga tcccgatccc aacccctttc tcctgggagt     480

gaaaccttag tttctaccag agagtgtggg aaaccacttc tggtggaagc ccct           534
```


<210> SEQ ID NO 348
<211> LENGTH: 580
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (109)..(109)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (241)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 348

```
aacattccct tgtcaaccaa gaatactcaa agctacttgt attggaaatg gcagaaggcc      60

taaatccaaa tttcttattt tttataattt accatagaag ttttgtgant aaattcttac     120

ttctgccagt ggaggtttat gcctgaaagg tcatggggtc ctgtctgtaa atagacctaa     180

agagaagtgc agtatttatt ctttgtaggc ataatgtgtt tgtcactgac aagcattcat     240

nttcatccca ctagtctttt attgcagtct tttattgtca ttttcagcct tatgttggag     300

agctttgctt tctcatcatg ttcacattgt cttaagtttt gtgagcttct gagaaagagc     360

ttggtaaagg tttaaagggg actttgttcc accaggagc attttatttg ggcgtctcac     420

ccttttctaa tgaaagctgt tgtaagccac ctctgacttg gaaattctga aagtatgaat     480
```

```
attttttata tcttaattgt aaaatgccag ttctccatta tttagatgaa tagtagaaca        540

ctgcaccctt tgtgcagtgt ttttgtttct ctactgcatt                              580


<210> SEQ ID NO 349
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

ccagtcttcc tggcaagggt aaacagatcc cctctcctca tccttcctct ttcctgtcaa         60

gtgcctcctt tggtgaaggt gacacatcat gtgacctctt cagtgaccac tctacggtgt        120

cgggccttga actactaccc ccagaacatc accatgaagt ggctgaagga taagcagcca        180

atggatgccg aggagttcga acctaaagac gtattgccca tgggggatgg gacctaccag        240

ggctggataa ccttggctgt acccctgggg aagagcaga gatatacgtg ccaggtggag         300

cacccaggcc tggatcagcc cctcattgtg atctggggta tgtgactgat gagagccagg        360

agctgagaaa atctattggg ggttgagagg agtgcctgag gagagccctc accgtctggc        420

accctagtca ttggagtcat cagtggaatt gctgtttttg tcgtcatctt gttcattgga        480

attttgttca taatattaag gaagaggcag ggttcaagag gagccatggg gcactacgtc        540

t                                                                        541


<210> SEQ ID NO 350
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

gaataaatct ctgggaccgg gtctcaccat attgctctgg ctggtttcaa actcctgggc         60

tcaagcgatc ctcctgcctc agccttccaa aaccaggtgt ttaacttggg actaacatga        120

agcacttaga agactacgtg gaacatagca atgactatat atgtactaca acgtaaacag        180

cacctcctgg attgaataga acataactga catgaccagc agagacaggc taaagacact        240

gagctgaaaa ccctggactc tattgctaaa ttgaggctcc tgaatccgtt cgctctgagc        300

aactgttgct gtggtgctgc cttcacaagc actctgctga gcactcagat agaggggctg        360

tgctatccgt caacagacaa gctgcagcca gaactgctca gctgacaaac tggta            415


<210> SEQ ID NO 351
<211> LENGTH: 438
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

gtggggaagc ctgaacacag tcctataaac taaaggccac tgcagacttt tagcacaagg         60

agatccttac agggaacatg tgccatcagc tctttggagt gaacaaggaa ttagaccccc        120

atcatgccaa aaaactagga tttttaggtg gtctttccat cccttcagat ttaagtattc        180

aaagaaagag agacagacct acattccaag ggtcttctga gtgcaaggcc ttgtgttgtt        240

tgtttatttta ggggagggcc tggtgctctt ctctgtttta tgctttacct tcttttattt       300

ctcagatctc atgttagcac tatgttctga attccctaat aatggctctt gagaactgat        360

ttacattttg ttggtttgtt tacttcttga gcacataaaa ggaccccaaa ttagagatac        420

tatcccttgg gcttctga                                                      438
```

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<210> SEQ ID NO 352
<211> LENGTH: 224
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

gtccactgct ggaaatagaa gttttttcgc tgcagggcaa ttctgtaaat gtgcttccca   60

gctttaggag gtctgaggct actcttctcc aataaccttc cttcccactg gaccttctca   120

ctcacagcac tgctgccctc tggacaagcc acagtggaca aatatgtcaa gctgaagatg   180

cacaaataat ttcaagttca gttctcaggg attcaaagga catg   224

<210> SEQ ID NO 353
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (177)..(177)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 353

tgtcctgggg atcttggagc ctgaattcat tggcacaaaa ggcagcagca tcctcactgt   60

atctgcagtc catttggact caataaaaac tttgaaagtc acatgtgtta tggaattcct   120

tctcagtgac acattcatct gtgctcagtt gtcccagcaa gggtcagccc ctcatanccc   180

tgcagcatcc gctgctatga agcagagctg taaacgccct ccctgtgtat aggaaaagct   240

acatggagca atcctcctg cctgaagaag tgcatctcag catcacttca gctgtcgggg   300

catttgtggg gagaaccaga ccacctctgc ggaaggcagc agaccctctt ccagccatgg   360

atggagttga attctctata aacggttcac cagcaaacca ccaatacatt ccatt   415

<210> SEQ ID NO 354
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

gccaggttaa tggtatcgat cctaatgggg attcggcaga gtttgatttg ttgtttgaaa   60

atgctttttga ccagtgggta gccagcacag cgtcagaaaa atgcaccttc ttccagatcc   120

tccaccatac ctgccagagg tacctcacgg acaggaagcc agagtttatt aactgccaat   180

ccaaaa   186

<210> SEQ ID NO 355
<211> LENGTH: 457
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

ctttacccta ggtcaggggt cagcaaacta ctgcctgtgg gccaaatttg cccaccacct   60

gtatctgtaa ataaggtttc attggaacac agctgtggcc atatgtttgt atattgtgtg   120

tggctgcttt tgcattagga tgacagaggt gaatagttgc aacagagact ggctggtctg   180

caaagcctaa aatatgtcct gtgtggccct ttacagaaaa agtttctaa ccctgctct   240

aggttacgga gaaaaaaaaa tggaataatg ttctctgcta cttttaacct gattttcttt   300

gtacctaaat aggcagctag aatgctgcct atatttaat aaggatttgg atctcacaag   360

acaccttagg cctacacaag ttgttcagat tctttgcccc agttctaatc tagtgacaaa   420

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ggcatagaat tctcctccca caggaatgta tttctat                              457


<210> SEQ ID NO 356
<211> LENGTH: 373
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 356

cagtctcctg ctcgtttaga agtaagggat aataatgtat ccatagctaa atgcccagtc     60

gttatatttt ctagatcaag atgcttgttg tgtacagttt cacagagcct tcggattttt    120

tctttaattt tgttcatgtc tttttcattc agtagcttgg ctgatgaagc atcttgttcc    180

agttccaaaa gtcgaatcat tagatccaag ctagctctat caagatccat gttcaaacga    240

tctctactca gtatatacat gagggcagct gtacagaggg acagattctg atggtgctgg    300

gaatcatcca aggtttttaaa gaccattgct accatcccat gtgctctcag gtgcattcgc    360

cagtaggcca aca                                                        373


<210> SEQ ID NO 357
<211> LENGTH: 116
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

tttgctccta acttgctctt ggacaggaac cagggaaaat gtgtagaggg catggtggag     60

aggctagaga tcctgatgat tggtctcgtc tggcgctcca tggatgcagg gagagg        116


<210> SEQ ID NO 358
<211> LENGTH: 522
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (297)..(297)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (418)..(418)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (483)..(483)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (486)..(486)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (490)..(490)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 358

gggcatctgg aattgacaca ccattacatt ctgtttgcag gatttttttt gtaaccatga     60

aattgaacat ttccaaatta taaactatgt taatacctat aaaatatata gccaggaacc    120

atttatcatc aagaaaagtg taagaaatta ttttttgagat gtaatttaag attgtttttat   180

gtaaaaggaa aatcttgtat ggcatcgaat agccttaatg aatttaattc tttcacaaaa    240

atgatttcaa attatcctag agtataacat ttttatcaaa gatattattt ccggagntct    300

tctttctttc tttttttttt tttttttagta atttagcaaa aacattactg ttctaatgct    360

gaagtgactt ttgccagtgc catgtccagg gggggaggta taagttactt gctcttanca    420

tttgggctgg attttttggt ttgggggaca cctttgggag tattcccaaa gcatgtctca    480
```

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agnggnggcn cccgagagca tggtttaaaa gcttggaccc ct                          522


<210> SEQ ID NO 359
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 359

gctgggccag tgcatctaac agccctgtgc agcagcttcc cttgcctcgt gtaacatgag      60

gcccattctt cactctgttt gaagaaaata gtcagtgttc ttagtagtgg gtttctattt     120

ngttggatga cttggagatt tatctctgtt tccttttaca attgttgaaa tgttcctttt     180

aatggatggt tgaattaact tcagcatcca agtttatgaa tcgtagttaa cgtatattgc     240

tgttaatata gtttaggagt aagagtcttg tttttttattc agattgggaa atccgttcta     300

ttttgtgaat ttgggacata ataacagcag tggagtaagt atttagaagt gtgaattcac     360

cgtgaaata                                                             369


<210> SEQ ID NO 360
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

agatactcag cactagacta acataacagg tcactacacg ggtgcagaat cactttacaa      60

aagaagactc tgttttacga aggggattca ctacagggac ttagagaaca gtctcttttc     120

tgcctttaaa atgagagttc ctccatttac caaaatttga cacgcacaca ttcttcaggg     180

gcatgccaat tgcgtaaagt gaggctcgcc tgcatagcta atcctgttaa agacaacttc     240

tcaaagcaca acgtgcttgt ttcctatcgg gctccctgcg gggctttctc tcactacaag     300

tcaagcttgg gctctcaaag ccctgcgcct gttaccacgg atgcccacag ggcctgggca     360

gttgctgtgg cgacagga                                                   378


<210> SEQ ID NO 361
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

acagtggatc aaatttaggc ttcttgatgc aggcatggtg tagattacta cttctgtatt      60

gtcccaggag ctcagcacat tccttgccag agatgataag gagctcaatc ttgaatactt     120

gttcaagctt ttgaataaaa aaccacagtt cctcaaagaa gaagaagaat tgcgaaatca     180

ccggaaataa ccgaaaactt ccccctgttt gactttcaac attcttgaat gcaccaagat     240

agcctctttc tgtgagatta ataaatgaat aaatgcctcc atattttca a                291


<210> SEQ ID NO 362
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (200)..(200)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

<400> SEQUENCE: 362

aagccggatg gcaaaagagc ccagaaccta ttggaactga caaaatcaag tcacggcgcc   60

tacaaagatg aggggcagat tctggctgcc ttttaatttc gtccttcacc tgatatctgt   120

gccagagaat gtcttccagg agttctgcta cagagaagag agtaacccccc atccatcatg   180

gccaaagcac ccagtcaggn tccgctctgg atccagcccg acaaatgcaa ccccttgaata   240

gggtttgtgc aagcaaactg gatgacgacc gaagaaaccc tgtcgcttct gagaagacac   300

ccaatccaag aat   313

<210> SEQ ID NO 363
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

cctggacccca actttgttac tgtgagaaag ggtcttcatt cattcaagat ggcatttgtt   60

aagcacctac tgctggagtg cagtggttca atcacggatc actgcagcct ccacctccca   120

gttcaagaaa ttctcatgtc tcagcctcct gagcagctag gattacagac aaaaccttgga   180

aatcaagaaa gttctggaat gatgaagctg ttcatgccaa gaccgaaagt gctggcccag   240

tatgagtcca ttcagttcat gccgtgacaa ttttcttgga actcctttt attgttagtt   300

ctcacttgtt tccatatt   318

<210> SEQ ID NO 364
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (117)..(117)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (119)..(119)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (153)..(153)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (155)..(155)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (241)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 364

ttagcatctt ggttactgga gaactataac ttttatgtag tcatgcttgg aaaacactaa   60

aagggaaatc gagtctgttt gacaatattc tgtcttcact gttgttcact tcataangng   120

tnggaatata aagttctata cagttaatat gangntctct ttagcattta aaacatgatt   180

tgcattttca tgaggcattt tggctaattt tattgatttc cttatatttc atagtcctta   240

nccttatgag aatcttatgt ttctgtgtgt tttctatcat gtagcacaat ttctgacaca   300

caaaacatac aataaacttg tgttaatttt tctatcaaag tcagaattta ttcataagga   360

atctgaagta aggtgtacta agcttgttta tgggttaagt gatatagcca aattcaaaac   420

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tttactttt  atgtcagtct  agaaatatct  cagattaaaa  catatcactt  cttagttcca        480

attagataag  ggaaatcttt  tataataatg  ccaggattgc  tataatctga  t                531
```

```
<210> SEQ ID NO 365
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (35)..(36)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (234)..(234)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 365
```

```
aggccatagt  aatcatcctg  ctgatattgc  aagtnngtng  ctagaatgag  gttatataat         60

atatacaaaa  acattttntc  aactgntaaa  gntgccttag  taatatgggg  taataccagc        120

aacattatgg  atatataatt  atagtctatt  gggccacact  taagtttgga  gtctaataaa        180

gtcacaatca  aattctgcaa  tttcaattga  agataacctt  gtctttatat  tatnaattag        240

aagctaaagt  tgatttttct  aagagttctt  tatttaaatg  aagtactctg  ggactgacct        300

tttcggaaat  ggaatcttca  ttggtcaggt  gattcaacat  ttttatacaa  tttatccatc        360

ctcatctctt  caggatttgc  ataccttgcc  agtttctact  ggccattgtt  gaaaatacat        420

ttatttggag  aagtccaaag  ccaaggggct  catgggctg   tgaggtcctt  cttgctgcat        480

cgtcctgtgg  tagaaggtgg  aggagtcaag  agagtgcccc  agagt                        525
```

```
<210> SEQ ID NO 366
<211> LENGTH: 267
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366
```

```
gggccaatga  aagcagggtc  aaggacagga  ccagcgcagg  ccaaggaagg  gaatatctga         60

cagcgcccac  ccagccaaac  cctcagccca  aggacaggaa  tgaggagatg  ctggtgaact        120

agccatccat  cagtacctgc  cttcccccga  ggctgcagcc  ccactcccag  gcgcctggcc        180

aggggagttt  tctaggttct  gagagccacg  ttgtcatccc  tgggctttga  agttaaacat        240

cacacagctg  tctataaaca  agatttt                                              267
```

```
<210> SEQ ID NO 367
<211> LENGTH: 199
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
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```
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(67)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (107)..(107)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 367

gattcaggga ttggatgagt ctctatggtt tgttttgccc tgaagagcag aaggcttctg      60

tcccaantgg tgttgccaaa gcaacatatt aattccatgc catgatnctg ggtcaagatn     120

tgcacaatct gattgggcat gtcacctcgg atggcaaggg agtggaagtg gtcaaaatca     180

tggagtccca gctttcgga                                                   199


<210> SEQ ID NO 368
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

gccccatgtt gcataggtgg cctataacca gtcagacaca ggagacaaca tgaagcccca      60

tctgtgcttc cctttctgac attaccacat ttgcctgatg gagtggccag ctccctttca     120

ctgctggaat gaatacaatc cagaaaacct accttctatt gctttaccta atggggtaag     180

gaaatttaag tagaaattgc taaccgaaga ctttgctaag caaacccagg tctgcttgat     240

gtcagagccc ttgctgttaa ccccatttac tgcttagcct ccaaagagaa gcaatagcat     300

cacatgggga aatgtcaaca gcataagagg actttcataa tcagaattta aactggctat     360

tatccctctg ga                                                         372


<210> SEQ ID NO 369
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

gaccgtgact cctgaagctt ttcagcgcag gtgtagccgg cttggcgtcg ccgcagtgag      60

gtttggagcc gctttggatt gctgagtcac tttcttcagc cacttaggga aaccgaaagt     120

ggaaactcgt ggggcttgaa atagtgtgtt ctcttgagaa ccaccgaggc agtgagattt     180

gggattccgg ggtctggaga tcgtgctttt tgtggactgc gtttgcagtt cctagggtgc     240

tgctgattca caggccttct ctgtctttaa gtgtgcagat cattgaccgc tcagtt         296


<210> SEQ ID NO 370
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

aaacccagag ccttctggat gtgtgaggta gtaggcttca accctcattc atgcataggt      60

cacacttctc caaagttggt atggcctgtc tccttggcat gttcccttgc ttctgcttgt     120

ccagttaatc ctttctgaca taccatgcat ctcagggtga agcggttgac atcagtaaac     180

tgtctccttc ttctagcttc atctgctaat tccagtgctt gtacaaga                  228
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<210> SEQ ID NO 371
<211> LENGTH: 206
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

cctcctgatc accatagctt tatgcaacaa caagaaacaa atttattagc taacctaacc      60

actaatgacg caagagacaa ttctaaggac tttcaaaaca gcaaagtagg agcagctgct     120

acctctaggg atgagggatg caattgtcca attattggtg aaattgtcat ttcatgctat     180

tggctatttg aaattcctcc tctaat                                         206


<210> SEQ ID NO 372
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (94)..(94)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (382)..(382)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 372

ccctgcctgt actaatgatc caaaaattag ccaggtgtgg tggtgcgtgt ctgtagtgcc      60

agctactcgg gaggctgagg caggagaatc tcangaaccc gggaggcgga ggttgcagtg     120

ngccgaggtt gcactactgc agtccagcct ggctctgtct tggtgttcag ccatgttccc     180

atgctcactc ccaaggtgac tctgggaagg tctcagcctt tttgtcttcc cagttaggat     240

ggtcccatgc ccctgttacc atcagacttg gtaagtttcc cgaggagact ctgcaagagg     300

cactgttctg gatggtggag gagagactag ttgttctgct ctcctggcca cagtgggtgc     360

agtggacccc atcatggaga anttcaacac atccagccta cgaccagcac ctgtgggagg     420

tggatattca aggcagcaga gcctacagcc ggggcatgga gaa                      463


<210> SEQ ID NO 373
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (87)..(88)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (231)..(231)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (406)..(408)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (421)..(421)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 373
```

```
agggtctcaa atgaactctg agttaccatc tttggacnga ctttttaatat aaagctgtaa        60

tccttaaatc tgtgtcagta gtcccannta ctatgtcact ttaattggat gaatgcgtta       120

atgaaaagtt tgttttcaaa cctcactaaa ctgctactta agatcacagt taatgtgagt       180

cctgcttaat ttggaaagca tttaaaaaat ggaaaagttt cttagggaag naaaaattt       240

gcaactctgc ctacaaggta cagtaattgg ctaggttctt ttgaagagca gtgttgacta       300

gagttaagga aaagtcagtt gtgaaaaatg gacatttta atagcaaaat gatgtgcttt       360

actgtagaaa caggaggaag ggtgcattat cctggggaaa atgaannntt cttcagttat       420

nttttatgct gctctacttt attgcaaaac g                                    451


<210> SEQ ID NO 374
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

cagtcaccga ccttccctga gattgctacc tggaagctct ttctat                       46


<210> SEQ ID NO 375
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

gaataagtac acagagtccc caaagactag tgaggccaag atgtgtgagt cattttccat        60

cacacacaaa aaacccaatt gttctaagta tgtattttac caagcagctt tatagaaaga       120

aaaacaaaca aacaaaccaa acaacaacaa caacaaaaaa ccttggccag gcacagtggc       180

ttacacctgt aatcccagca ttttgggaga ttcaggcggg tggatccttt gagcttggga       240

gtttgagatc agcctgggta atgtggcgaa acctcatctc taccaaaaat ataaaaacta       300

gccaggtgtg gtggtgcacg cctgtagtcc cagctgctta ggaaactgag gtgggaagat       360

tgcctgagcc caagaggtag aggtttcagt gagccgtggg aagattgcct gagcccaaga       420

ggtagaggtt tcagtgagcc gtgggaagat tgcctgagcc caagaggtag aggtttcagt       480

gagccaagat tgtatcactg cacaactgtt gcctgggca                               519


<210> SEQ ID NO 376
<211> LENGTH: 222
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

cctgctggac agccgcgcag gatgagccgg agaccccgag ggccgtggcc ttccaggact        60

gccccgtgga cctgttcttt gtgctggaca cctctgagag cgtggccctg aggctgaagc       120

cctacggggc cctcgtggac aaagtcaagt ccttcaccaa gcgcttcatc gacaacctga       180

gggacaggta ctaccgctgt gaccgaaacc tggtgtggaa cg                          222


<210> SEQ ID NO 377
<211> LENGTH: 460
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

atagtagggg caattttgtc tgtagatggc agtatgacaa ttcttgctag agaatatatt        60

gaaaaaaact tcaacacaaa gggttgtagc actgtcctca gtaccattgt gtgcatgagg       120
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atcagaatag tctgggctag atacatcaca ttaaagcttt tcagaatctg ataaatagct      180

ctaaatacta atgatattga gaagcctagc ttcacttggg aaaatctgtg gctgttcaca      240

gaaattcagc accaagttat tccccccata ctctaccagg ccttcaggtc ctcataaaga      300

aaagtgtcgt tttcagatta ggaactcaaa attattttgg tgcatcaaat ctacagtcac      360

acaatataac aagaatggga ttagaaaaat gaaagcctac tcattctcat ctttaagcca      420

gagaatgaaa tatatatgag gtctctggat agctatttaa                           460


<210> SEQ ID NO 378
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

cgccgcatca agccgtggcg gagatcgacg cgctctacga cgtgtacctg gacgtgatcg       60

acaagtgggg caccgacgac atgctgttcc tgggcgactt caacgccgac tgcagctatg      120

tgcgggcgca ggactgggcc gccatccgtc tgaggagcag tgaggtcttc aagtggctca      180

tccctgacag cgccgacacc acggtgggca actcagactg cgcctacgac cgcattgtgg      240

cctgtggcgc ccgcctgcgc cggagcctga agccccagtc ggccaccgtg cacgacttcc      300

aggaggaatt cggcctggac cagactcagg ctcttgccat cagcgaccac tttccagtgg      360

aggtgaccct caagttccac cgatgactcg aggcctgact ggggcatgcc acctgcagac      420

cctggctctg aggaatggcc caacagtggc cccttcaggg tggcagccac ccttcagtga      480

ggccccaagg cagagtcggc tgggcgtgga ccaggggcat ggacacgtga tgtgctgctc      540

tgta                                                                  544


<210> SEQ ID NO 379
<211> LENGTH: 254
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

gaagtttgtc ttcctacaac cacgtgatcc tctctctggg atttccccac tcaaccaggg       60

acaagaggtc aaagttgacc tgattatgtg tccatcaagg aagtgcccct ggaaggcaaa      120

taaagaaggc accatttaca ttacagtctc ctaagtgcag gcaatgatac cccaaggtgg      180

ggctctgcag accctccagc aaagagcttt tgaaaataaa tgtgaagctg ggcttaggag      240

ctcatgcctg caat                                                       254


<210> SEQ ID NO 380
<211> LENGTH: 398
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (140)..(140)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (295)..(295)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 380

aacctgctaa ccaagaatgc tttacctggc aaagctgtcc ttcagaaatg agggagaaat       60

gaaagctttc tcagacaaac aaaaacaaag gaaacatgta aaagtgaaaa aataaatggt      120
```

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```
ataagtaata tatagtcccn actcagaatt ctctaatact gttaaggtgg tgtgtgaagc        180

aatcttatta ctactaggag ggttaagaga caaaactatt aaaaacaact gcagctacag        240

tatattgtta aaggacacaa attttaagtt tacatcaaaa tcagaaaaca tgggnaagga        300

aggaatgaaa gtgcagagtt tttgtatgtg attaaaggca aattgttatc agtttaaagc        360

ctgttttaag gataaaatat tttatgtaag cctcatgg                                 398


<210> SEQ ID NO 381
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

cccgccgcgc gagattaaag gacagaccaa gagggcgcgg gagctaccag cttggagggg         60

aggacagatg gggacccagg gctggccagg gctggtctct ggagctgttc tgccagagtg        120

atggggcgc ttggcgaggc caaggatttg gttgggtcct atctctgaga cattttgaag         180

tctcacaccc cttccatttg ttgcctattc cacttaactt tgtatttgtt tgaaatctac        240

tgttcggatg ctggactaga agagggacac ttggcc                                   276


<210> SEQ ID NO 382
<211> LENGTH: 119
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

aaacataaca gaggagttgc gaattttatg aaatttctga gtcttacaaa cttctcttta         60

agactatgag gaaatgctga cttgtattat ttatatcatt aaatttgctt gtgtatggt        119


<210> SEQ ID NO 383
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

gtccctgctg tttagtatgc tggagtggag gttctgtgac ttcctgttta gtggtgctga         60

ttctagttgg tgtgaaacgt cagatttcat cccagtcgcg tggctgattt ttttatgtgt        120

ggttctctgt gtttccagcc tggtcctgct ggtcaggatc ctctgtggat cccggaagat        180

gccgctgacc aggctgtacg tgaccatcct gctcacagtg ctggtcttcc tcctctgcgg        240

cctgcccttc ggcattctgg gggccctaat ttacaggatg cacctgaatt tggaagtctt        300

atattgtcat gtttatctgg tttgcatgtc cctgtcctct ctaaacagta gtgccaaccc        360

catcatttac ttcttcgtgg gctcctttag gcagcgtcaa aataggcaga acctgaagct        420

ggttctccag agggctctgc aggacaagcc tgaggtggat aaaggtgaag ggcagcttcc        480

tgaggaaagc                                                               490


<210> SEQ ID NO 384
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(73)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

<400> SEQUENCE: 384

```
gatacctcat tatacatctt acagagagca tcattggtgt ttccaaggtc acagggctag        60

gcaagggtgg anncctgagt ctgcttgtct gtttgcccca tgacagccca ggggtggtgg       120

cctcactcca cctccaggca cccacaagaa tataaaatct tgtacaagga tgtcgatatt       180

actattgcca ttcccaagtg cacctgcacc tgtagtatca ggtggtttnc agccttggct       240

gcatagctgc atatgagaat cacctgggaa gcttttaaag atcccagtat ccccacctct       300

tccccagtta cagtggagtc ttgcgggtgg tggggggacat cattattttt gaagcttcca       360

agtaattctg gtgtgcagtg gggtgaccag ctgtcccagg gacctccttt aaaaaataat       420

atcccgggca catgacaggc caattgccct aatgcaac                                458
```

<210> SEQ ID NO 385
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (343)..(343)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (467)..(467)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (471)..(476)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 385

```
cacctctgca cttttgtagg ctcaacaagt actggggagc ctgccaccac tgtatgcctt        60

tgaggcccct gccctgcctc cctggctggc cacggagctc gccctccctg gtaggggggtg       120

agtttggaag tgagaggctg gtgtgggtct gtcccatgag ctgactcaca cttgcctcac       180

cacacatacc atcagaagac ccacgtggtg gagctaccgc tgctgctccc cacagtgcac       240

ctaggcacccc tcctgtcctt cccatggcac tcggttgacc tgggggttcc tgtccaacag       300

gtgaggcctg gtgtgcacag acactctgcc attgctagaa ggnggctgtg ccccctgcta       360

agatatcagt aggtccttca cagcctcacc ttgttcctcc catttgtttt taaaaattgt       420

ttcttatata tacagtttat ttagcttacg taaacatttg gtgcacntaa nnnnnntcaa       480

agatcatgat gtctcttttg tggttttata                                        510
```

<210> SEQ ID NO 386
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

```
cctctgccat tgcccaaaga aagtacgcag gagggaaggc gccgggggcg caggagtcgg        60

ggggaagtga aatctcggca ttagaacccc cg                                       92
```

<210> SEQ ID NO 387
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

```
aaggcgccgt caagtcaaat aaataaatgc cctacaacac caacccagga ctgagatctg        60
```

```
catgctggaa tgacggtggt ggtggtggct ttcagtattc cccaggtttt gtccggagca          120

ccggcacgcc ctctcttgaa gtccgctctc cgcacagtgg ttagacggga agatccggag          180

ctgtccagtg tcttgggtaa tgcacggcat cgcctgatgt ctgacgctag aacaccacgt          240

aaagtcaagc agagggaagt gaatgcgccc taggcccctg caggccacca agaagagcta          300

gagggagttg gtgcaatcct agagatgccg gcaggtgcac caatctgtgg cacacgtacg          360

ctctccaatg gaagacaact caagaccaca ccaa                                      394


<210> SEQ ID NO 388
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

actataatgc acttcgcaaa atgtaagggg ccggcttcac gccagcgggg ccttctggga          60

ctttgaattc aaccaggtga gcgctccagg tgccccgaca ggcgcactgt agccactggg          120

tgttaggggc gggagtctgg aaggtgacgg tagacggcca cttgggccct tctgggggcg          180

agcctactgg tggggtcagg gctctccgtg ctcagagcaa ggtagaggag caaggcccta          240

cttttggggg gcagggtcca gaccaaggac cctatgcgcg gagggtggc                       289


<210> SEQ ID NO 389
<211> LENGTH: 139
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 389

aggcctgacc gaagagaact ttaaggaact aaagcaagac atttctagtt tccgctttga          60

agtcctggga ttactaagag gaagcaaact ttccacaata caatctgcga atgcctcgaa          120

ggagtcttca aattcggca                                                       139


<210> SEQ ID NO 390
<211> LENGTH: 528
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

caggttcttg aagttctcca ccatgacatc tcggtacagc ttcctctggg taagatcgag          60

cagtcgcagt tcctccctgg agaagaccac agccacatcc ttgaatgtca cagcctccta          120

caatatcaaa cacatgtaac ctcaatctta caaccaacct tcactagaag aagggtggca          180

tcaagaagga aaagagcacc acaaaaaagt tgttatagat tccaagagat ctcagtcaat          240

tttcagctgt tacagttttc cctgtctcac tatctcctac gctcatcccc ataaagcctg          300

tagtttatca ctgttttttg ttttttttctt ttttgagatg gagtctcact ctgtcaccca          360

ctgcactcca gcctgggtga caggggtgag acactgtctt aaaataaata aattttaga           420

attaaaataa atagatcata aagtgtttga aaggatcaga tgaatgaata tatgtcaagc          480

acttagaagt gcctagcaca ccatacatgc tcaataaact cgaacaac                       528


<210> SEQ ID NO 391
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

gccaggggtc gccaatcctg gaaccccact ggcttagagg gctggggggag agaaacatgc         60
```

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```
tgccctcttt gtagcagtca ggcgctgacc caagagaact caccttattc ttcatttcgc      120

ctggtaatcc tccaggccct tctctacacc ctgaagggga gggaggaaaa tggatgaatg      180

agagagggag ggaacagtgc ccaagcgctt ggcctctcct tctcttcctt cactttgcag      240

aggctggaag acggcagccg ccggactggg cagatcctca agcagaccta cagcaagttt      300

gacacaaact cacacaacca tgacgcactg ctcaagaact acgggctgct ctactgcttc      360

aggaaggaca tggacaaggt cgagacattc ctgcgcatgg tgcagtgccg ctctgtagag      420

ggtagctgtg gcttctaggt gcc                                             443
```

```
<210> SEQ ID NO 392
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

tattggcacg tagcagtaca aggatggtga ggggtgggta gggggcagac agctaggcac       60

ttgaaaggaa agctcatctg gaaagattgg atcgtctcaa atgcacatac tcgtacactc      120

gattgaagcg tactctgtgc ctactagatc ttttcacagc caaaaacacc tggcaaccct      180

tggagaagta actattcctt tttttcacaa gtaagaaaat agagcctcag aaaatttaac      240

agttgtctaa gctagaaagt agcaggactg gactttgaag tagtctttag gttgtgctgt      300

acattttgtg gatatgctta aatcacagtt tagcttgtac acattttcct ttattagaat      360

tggaagtaag tattaatgtt tgaaaaaata ttttagcctg acaatattta ttctatcttc      420

atatgttttt gaaattagat attttaaact aggcacggtg gct                      463
```

```
<210> SEQ ID NO 393
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (99)..(99)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (123)..(123)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 393

agctcatttt agtctcattt ctctcnctcc cttcttccct gatgaataaa gtttattggg       60

atggntttca gatgctcagc ttttccatat gattaggtna gtgatccaga acccttccaa      120

agnaccctgt ggactcaacc ctctgtttga acaacataca agataatatg agacatttat      180

ttatcgagga ccctctgagc acctggcact gtgccagatt ctttcagata tataaaattt      240

cacttgctcc tgttgattct ggaaaggagc aacggcatct tatgaagctg tagcagatac      300

tgtcctggcc tcgctcatgt gtgtcagatg tgttggagtg ccctggctgc tgctctgcat      360

gtgtagctga ggtcct                                                     376
```

```
<210> SEQ ID NO 394
```

-continued

```
<211> LENGTH: 220
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

tggattcatg ccaaaggaaa ctgaaagcct gcctttcttt ttttcccagt gcacatctca      60

gattatttgg cctttgtccg aggactgaaa acagttctgt gtccaagtat gttttaata      120

cctgatattt atttcacaaa aaaactgaaa ttgctttgtg tgtccaggct tgaatgttta      180

aggcatactt gattaataca tgtgtgctga gtgcttcctg                          220


<210> SEQ ID NO 395
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

caaccgccac atagtcacat tgtcaaatag cgtattcacc ttctcttata agaaggctca      60

gcgagatctg gcgtataagc cactctacag ctgggaggaa gccaagcaga aaacggtgga      120

gtgggttggt tcccttgtgg accggcacaa ggagaccctg aagtccaaga ctcagtgatt      180

taaggatgac agagatgtgc atgtgggtat tgttaggaga tgtcatcaag ctccaccctc      240

ctggcctcat acagaaagtg acaagggcac aagctcaggt cctgctgcct ccctttcata      300

caatggccaa cttattgtat tcctcatgtc atcaaaacct gcgcagtcat tggcccaaca      360

agaaggtttc tgtcctaatc atataccaga ggaaagacca tgtggtttgc tgttaccaaa      420

tctcagtagc tgattctgaa caatttaggg actcttttaa cttgagggtc gtttttgacta      480

ctagagctcc atttctactc ttaaatgaga aaggatttcc tttcttttta atcttccatt      540

ccttcacata gtt                                                        553


<210> SEQ ID NO 396
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (103)..(103)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (111)..(111)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (114)..(114)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (132)..(132)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 396

ctagaaactc actcagtcct gtggttgcca acctttctcc atctcccgca gacgttttac      60

tgcatgccag ataccatgtg cagtaacttn tgaatcctct canccccta nctnccagaa      120

cacnggacta tnagttactt gaaagctgag gcttggtaga gggctggagc caattgcgtt      180
```

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```
aaactaacta acattattgc aaaatatatt ctagggcttt tactctaata aaaatgactc      240

ctggaactgc agtactatat tcttggaacc ccaagaaacc aggtgacaac ccataaattt      300

accatcactt ttcagatgag gaaggcaaat ctggaaggcc aaattacttg tccaaag        357
```

```
<210> SEQ ID NO 397
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (184)..(184)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (350)..(350)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 397
```

```
gttagcacat accattgaat tcactgagac acatgagaaa atatgggaaa gtcggagagt       60

ggaagtaaat gtaaagaccc ccctcctccc caaagagtac gttgtgtagt ggggtagagt      120

ggaaaatcaa tccaagaaaa gtagcaaacg gacccaaaga tgaagaggaa gaaaagaaac      180

agcnacacga aacgnaaaaa aaaagccacc agatttgttg caacgttgat gtaaacctgg      240

ccgtcttcct gaaccagtga cccagggttt ccgcttccct ttgctgtcat cttgctcaag      300

tctagaagct gaaatatcat catcaactcg acatgagggg ataacctctn gatccactca      360

tcagatgctc atcagacgtt ccaattacaa aactgaacct cttcttagtg ctggggcggt      420

tag                                                                   423
```

```
<210> SEQ ID NO 398
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (132)..(132)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (150)..(150)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 398
```

```
ggacaaaaac tttcccaagt cagctttta ctatgattac gtcctagcct cagatgtggt        60

ctaccatcac tacttcctgg acaagctgct caccaccatg gtgtaccttt cccagccagg      120

gacggtgctg cnttgggcaa acaaattcan ggttcagcac cgactatgaa tttttagata      180

aattcaagca agtttttgac acaacactgt tggctgaata tccagagtca tcagtcaaac      240

tttttaaggg gatactaaaa tgggactaaa tccaacaaaa tgcctttcac aacgttactg      300

tgtcttttga gcaatgtgtt agaaattgct ttggtaatag acttctttca caggattgag      360

aaggtagtgc atagaaacaa cttgtatact tggaacaaat gtaacaatac tgcagaaact      420

ttctaatttc taagataatt taagattatc tggttaatct aaatatctaa aaagaacaac      480

ataaaaacat gaaagtagct ttgttggttc caacg                                515
```

```
<210> SEQ ID NO 399
```

-continued

```
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(60)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (62)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(85)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (88)..(88)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (134)..(134)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (278)..(278)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (304)..(304)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 399

gactgccatc tgatcaacag ctacccttca gccaatttca cctttctgtt acttnnnnnn      60

anngngccct tgtgtggata atgtncancn cantaaggaa tgcatgttag gtactttaag     120

tcccagtaga atancagttc ataatatcac acatgtggtg aaatctaaaa aggcaatagg     180

gctaattttg gcaggagttg gaatagcccc ttgggatggc tttgcatact gtcagacagc     240

tttgagaaac tttcaaaccc ttgaaacact ggcaactnag tacaggcaga gccataaaag     300

gacntcaagc ctccctgcac tccctagcca atgctgtctt ggataacaga tttgccctgg     360

aatatcttct ggctgaacaa gggcgggtat gcacagtaat aaaccacatc tgttgttctt     420

acattaacag ttcaggattg gctaaactgc aagttcaaaa gatttaccaa gaccaggcac     480

aat                                                                   483


<210> SEQ ID NO 400
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (483)..(483)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 400

ggagcaaaac acttggaacc cacaagactc ccagaaggtg aagttaagag ctcccagact      60

cataaggtta ttagaacagc aaactggcac cccaaagaac tttacggaga cttgcaacct     120
```

-continued

```
atcaacaagt tggatgaggg attaaaagcc ttcaacaacc aacaacccca agcatcaaac      180

tgaaggaaac attctaacct tcacagacag actggaggct ggatggggac ctggctgaag      240

acatctggag aatgaaagtt aagtaccagc ttgcattttt gtgcccctag attatttttg      300

cattttaaaa taagaagcat caaattgcgt gtctctgtgt aaaagttcta gcaatttgtt      360

ttaaggtgaa cttattttgg cttagggact acaaaaagag aaggtaattc ctagggaagg      420

aagaagagaa agaaatgaaa attagagaat aagattattt tgaatgactt caggtagcga      480

ggngtgtgtg tttgtgagtg tgtatttgag agacttggct catgcctgtg ggtcttctct      540

tctagtatca gtgag                                                       555
```

```
<210> SEQ ID NO 401
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 401

ggctgagaaa ctactggagc accagggaca gtctgtaaag ttggatggac caccaatggg       60

aaaatgagag ctgcccaccc tggccttaca ctccttcaat taatacataa acagaaagga      120

ggatatacag agagccaaag gcccatggga cgtgaccaac attccactga gtctatacga      180

tcaaacagca aactgtttat catgaataca gaatgtgggc aaactcatga ctgtgcctgc      240

cccagaaggt ttgctgaggg caattgcttc ctgacgccaa gctccttgag gttatctatt      300

gggacatcca gagaatgcag tcttgca                                          327
```

```
<210> SEQ ID NO 402
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

gggtggcctg gggatagtgg cttcatcttt tggggcttca agattctttg tctttaaaat       60

caggggttat atcaagatca tcaaagttcc cattccatta aagaaaaccc tgcatgtatc      120

cataatgatg cttcttcctg ttaaatttac aatgaaggga aacccatcac ttaactgtag      180

gaatttccca aaatgaactg atgaccagtg atctctctat cagaaaatgg cagatttcta      240

gccttccaga actttgattt tcttggacat tcaatggttc ctttttccca aatatttttc      300

aactgatgcc aaaccttgga tttggtttaa tccacctttg gtttaggttt ggggaccctt      360

ttcctggacc gtcccagttt tgggttaaac cgatttggat gaccctgtga gtcgccactg      420

gataccgaca gtctgctgtg gtgcttagaa gccactgaaa cattggtgaa tgtgaagtca      480

cttttggggt gcctgcc                                                     497
```

```
<210> SEQ ID NO 403
<211> LENGTH: 512
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

gaaagctcca atccatgac agtcgaagtc tctgctcctt caggaacagg acatcttcct       60

ggccttaatc cattatagca gccgtgatgt catttctgta tttcaggaag actggcagac      120

agttgctttc attcttcctc aaagtattta ccatcagcta cagtccaaaa ttgctttttg      180

ttcaaggaga tttatgaaaa gactctgaca aggactcttg aatacaagtt cctgataact      240
```

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```
tcaagatcat accactggac taagaacttt caaaatttta atgaacaggc tgatacttca        300

tgaaattcaa gacaaagaaa aaaacccaat tttattggac taaatagtca aaacaatgtt        360

ttcataattt tctatttgaa aatgtgctga ttctttgaat gttttattct ccagatttat        420

gcactttttt tcttcagcaa ttggtaaagt atacttttgt aaacaaaaat tgaaacattt        480

gcttttgctc cctaagtgcc ccagaattgg ga                                     512


<210> SEQ ID NO 404
<211> LENGTH: 229
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

cacccattc aaactcaagc acagtatgcc tccccagtct ttatgcagcc tgtatataat         60

cctcaccaac agtactcggt ctatagtatt gtgcctcagt cttggtctcc aaatcctaca       120

ccttactttg aaacaccact ggctcccttt cccaatggta gttttgtgaa tggctttaat       180

tcgccaggat cttataaaac aaatgctgct gctatgaata tgggtcgac                   229


<210> SEQ ID NO 405
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

acagctcagg ttttatcacc gactgggaat agacaacctc aatgctgaac cgcactggag         60

aaaaggggca aggtacccct gctgaggtgt atgggctgcc atctcaggct gtcttgagga       120

cctgggctcc ctctgctact cccaggaaat gggctcctga cacagcagtc tgccaccaca       180

gccccaggag ggtgtcaaca ccagcaaatg ctgtatttgc agcatgtcca agatgaccct       240

tctcccctac ctctacctag ccactggcag ggaggggaga cagtggtgat agcagcagca       300

ctctaggcat ggtgaacgcc tgggaccaag ccatgtggcg ttttttattt tgcctttctg       360

gaagactcaa gatatgtctc ttcattctct ctcagtattt gtttactttg gttttttttgt      420

ttttaatctc agagagaggt gtgtttagtg ggcacaagct gtaatattca gcaaaacttt       480

gtcgactggc actgt                                                        495


<210> SEQ ID NO 406
<211> LENGTH: 472
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (77)..(77)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (79)..(79)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 406

ttcctcttgc tgagaaaacc caccctgctc acctaaaccc tggccttgcc tggtaattcc         60

atccatgcgc ctggaangnc ccagacatca aggctctgag gggccaggca cggggagaac       120

ccagcagtgc cctgccctgc agtctgagct accagattcc ttgtgaagat aatttgagga       180

ccatgactca cccaaccaca tttcctgggg cctcaaattg aaaattcagg atgggctttt       240

ctatatgact ggctgatatc caactatgcc atggtcttta catgccatga acattctttc       300

ctgccagagt tctaagaatc tgtgttctct gccttagacc ttctgcagat gagcccacag       360
```

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```
gaagctccac gtgtagctga gctacatgca ccaggcctca gtttgcccca agtccctgt      420

gtactctctc atggcctgtg ccaagaaat gtattctctc actttggact ta             472


<210> SEQ ID NO 407
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

agcagatgga ccctactgga agtcagttgg attcagattt ctctcagcaa gatactcctt      60

gcctgataat tgaagattct cagcctgaaa gccaggttct agaggatgat tctggttctc     120

acttcagtat gctatctcga caccttccta atctccagac gcacaaagaa aatcctgtgt     180

tggatgttgt gtccaatcct gaacaaacag ctggagaaga acgaggagac ggtaatagtg     240

ggttcaatga acatttgaaa gaaaacaagg ttgcagaccc tgtggattct tctaacttgg     300

acacatgtgg ttccatcagt caggtcattg agcagttacc tcagccaaac aggacaagca     360

gtgttctggg aatgtcagtg gaatctgctc ctgct                                395


<210> SEQ ID NO 408
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

attttcctca taaagcattg ctccagctaa tcttatctat ttttctccag aatctccatc      60

cccttcccgt cagatacatc taaaactttt tttgtatctt tgttttttcct cgtgttgtat     120

catcttccta aaacatgttc tacttgtgaa aaccctaaga aattctctct gtcttattga     180

aattctatct ccactgtgaa gcattatcat ggtgtggcca tatatgatct atccctatct     240

gaagtcactg catttattcc ctgatcctca tttgcaggtc cagtaccttg tacaagtttc     300

tttttgtgcc atattagact gtaagctcca agagggcagg gcccaagtct tatgaatttg     360

tgtctgcata gtgtctagta cttgtctgag gcccaca                               397


<210> SEQ ID NO 409
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 409

aggacgtacc ttgtgagatg cgagccggcc aacagcttgc aagcatgc                    48


<210> SEQ ID NO 410
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 410

gcaagtcgcg tgatttctac cacacctgct actgcctgag cggcctgtcc atagcccagc      60

acttcggcag cggagccatg ttgcatgatg tggtcctggg tgtgcccgaa aacgctctgc     120

agcccactca cccagtgtac aacattggac cagacaaggt gatccaggcc actacatact     180

ttctacagaa gccagtccca ggttttgagg agcttaagga tgagacatcg gcagagcctg     240

caaccgacta gaggacctgg gtcccggcag ctctttgctc acccatctcc ccagtcagac     300

aaggtttata cgtttcaata catactgcat tctgtgctac acaagcctta gcctcagtgg     360
```

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```
agctgtggtt ctcttggtac tttcttgtca aacaaaacca atggctctgg gtttggagaa      420

cacagtggct ggtttttaaaa ttctttccac acctgtcaa                            459


<210> SEQ ID NO 411
<211> LENGTH: 275
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 411

agagggcaag gggctggatg caggcagaga atgactttaa gaaaagattc tatgatccct      60

tcctttagta tggagctcga ttttccagct ggcgcttggt gagaaagtac ttgaagaact     120

catagacaga ccaagaaatg gcggtggagg gcatctggta gatgacacgc gcctggatgc     180

ctttgaagta gccggccagg ccgttgagct ggtacaccgt ccggaaggca ttggccatac     240

ccgacagccg gccgctgatg ttggccagcg agagg                                275


<210> SEQ ID NO 412
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 412

gcagataagc tccgtctgca gttccaggcc agccagaaac tcctgtgtcc acatagagct      60

gacgtgagaa atatctttca gcccaggaga gagggggtcct gatcttaacc ctttcctggg    120

tctcagacaa ctcagaaggt tggggggata ccagagaggt ggtggaatag gaccgcccccc    180

tccttacttg tgggatcaaa tgctgtaatg gtggaggtgt gggcagagga gggaggcaag    240

tgtcctttga aagttgtgag agctcagagt ttctggggtc ctcattagga gcccccatcc    300

ctgtgttccc caagaattca gagaacagca ctggggctgg aatgatcttt aatgggccca    360

aggccaacag gcatatgcct cactactgcc tggagaaggg agagattcag gtcctccagc    420

agcctccctc acccagtatg tttttacagat tacgggggga ccgggtgagc cagtgacccc    480

ctgcagcccc cagcttcagg cctcagtgtc tgccagtcaa gcttcacagg cattgt        536


<210> SEQ ID NO 413
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 413

ttaatttctg tgaagagtgc ccctggtgtt tcatcttggc ctgttttgat gagaatgtta      60

tcntttgtgt ctggataacg cgtcagcttc ttaaagtaca tataaagata ttctgtcacc     120

nccccacatg cacacacttt taaaatctat ttttattctc ttgctaaagt tgtaattatg     180

tcaagaattt tccagctcta actgccttct tagtacatgt ctttctgcct ttgaagcata     240

tgagtttgcc aaagtcattc tcccctaatg acatattgtg gactta                    286


<210> SEQ ID NO 414
<211> LENGTH: 166
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 414

gaaagacgga ggaaacaatc aaaatcncca ttctattgct ttgacacctt tactaggtga      60

attggtggca ttcncaaagc taatagggac gtttatatca agaaacattt ctgtatatat     120

tgttgaattt tagttgtaca tatactttgt atgtttttgt cttctt                    166


<210> SEQ ID NO 415
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 415

tgcaggctag gggaggagcc accccgctt  ccctattgtg accaggccta tggggaggag      60

ctgtccatac gccaccgtga gacctgggcc tggctctcaa ggacagacac cgcctggcct     120

ggtgctccag gggtgaagca ggccagaatc ctgggggagc tgctcctggt ttgagctgca     180

ttcaggaagt gcgggacatg gtaggggagg caaaaagcct tgggcactac cctccctgtg     240

gagctgttcg gtgtccgtcg agctagccac accctgacac catgttcaag ggtaccggaa     300

gagaagggtg tctgccccca acctcccctg tgggtgtcac tggccagatg tcatgaggga     360

agcaggcctt gtgagtggac actgaccatg agtccctggg gggagtgatc ccccaggcat     420

cgtgtgccat gttgcacttc tgcccaggca gcagggtggg tgggtaccat gggtgcccac     480

ccctccacca catgggccc  caaagcactg caggccaagc agggcaaccc cacacccttg     540

acataaaagc at                                                         552


<210> SEQ ID NO 416
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

acgccgcgcg aaggtgatga gctcgcccgg ctgccctacc tacggacctg gttccgcacc      60

cgcagcgcca tcatcctgca cctcagcaac ggcagcgtgc agatcaactt cttccaggat     120

cacaccaagc tcatcttgtg cccactgatg gcagccgtga cctacatcga cgagaagcgg     180

gacttccgca cataccgcct gagtctcctg gaggagtacg gctgctgcaa ggagctggcc     240

agccggctcc gctacgcccg cactatggtg gacaagctgc tgagctcacg ctcggccagc     300

aaccgtctca aggcctccta atagctgccc tcccctccgg actggtgccc tcctcactcc     360

cacctgcatc tggggcccat actggttggc tcccgcggtg ccatgtctgc agtgtgcccc     420

ccagccccgg tggctgggca gagctgcatc atccttgcag gtgggggttg ctgtataagt     480

tatttttgta catgttcggg tgtgggttct acagacttgt cccc                     524


<210> SEQ ID NO 417
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417
```

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```
aaatgactgc attcgtctct tttttaaagg tagagattaa actgtataga cagcataggg      60

atgaaaggaa ccaagcgttt ctgtgggatt gagactggta cgtgtacgat gaacctgctg     120

ctttgttttc tgagaagagg tttgaagaca ttttattaac agcttaattt ttctctttta     180

ctccatagga acttatttta atagtaacat taacaacaag aatactaaga ctgtttggga     240

attttaaaaa gctactagtg agaaaccaaa tgataggttg tagagcctga tgactccaaa     300

caaagccatc acccgcattc ttcctccttc ttctggtgct acagctccaa gggcccttca     360

ccttcatgtc tgaaatgg                                                    378
```

```
<210> SEQ ID NO 418
<211> LENGTH: 116
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

agtatggaag ctgagaagag ttattggaat cacccccacc gttgacagag gaaggcaggg      60

ggtgagaatt aactgcttga gggtaggaga gtctgagatg tgggggccct attccg         116
```

```
<210> SEQ ID NO 419
<211> LENGTH: 147
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

cctgagccac cacgcagaag aggcactttc caagttgttt accaagaatt tacattaaaa      60

taacaagcta ttgtttggct atacattgtt ctttgtatca catattccag gaactacagg     120

aaaataatgg gtgaggcagc tagttag                                         147
```

```
<210> SEQ ID NO 420
<211> LENGTH: 310
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

gaaattccat caatacatct agacagatgt ttgcttgtag tttttggtat ccaaaacctt      60

ttttccacac atcgcacaga tgcctttttt gtaggcacag ccctggcagt aatgagaacc     120

tggttggtgc acagaacttt tacaaattct acaagtggag aacttattct ttccatatgg     180

atcaaatctt gctttttttg aagtcaaagc tttattttca ttcagctttc ttccaccact     240

ttctgtggta ttcctagcac cacctttcca tgtatctgga gtgataacag taccaagttt     300

cttttcacat                                                            310
```

```
<210> SEQ ID NO 421
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 421

agatataact ggtagagcac gtcaaagata tacagaaata accagagaaa agtttgaggc      60

attaaaanaa gaaaatatgg acctaaacaa tatgaatcaa agccttaccc ttgaactaaa     120

cacaatgaaa caagcaatga aagaactaca gtta                                 154
```

```
<210> SEQ ID NO 422
<211> LENGTH: 444
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 422

ttttttgtgca tgattacact ccactgacat cttccaagta ctgcatgtga ttgaataaga      60

aacaagaaag tgaccacacc aaagcctccc tnggctggtg tacagggatc aggtccacag     120

tggtgcagat tcaaccacca cccagggagt gcttgcagac tctgcataga tgttgctgca     180

tgcgtcccat gtgcctgtca gaatggcagt gtttaattct cttgaaagaa agttatttgc     240

tcactatccc cagcctcaag gagnccaagg aagagtcatt cacatggaag gtccgggact     300

ggtcagccac tctgactttt ctaccacatt aaattctcca ttacatctca ctattggtaa     360

tggcttaagt gtaaagagcc atgatgtgta tattaagcta tgtgccacat atttattttt     420

agactctcca cagcattcat gtca                                            444


<210> SEQ ID NO 423
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (357)..(357)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (454)..(454)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (462)..(462)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 423

gctttggact ggctcgcatg gaaaaccagg catttgatcc cgagaaaggg aacttcaaca      60

ctttgttttg caggctctgc gtgctgctgc tggtgtgtgc cgcccaggcc tggctcatgt     120

ggcgcttcat ccactcccag ctgcggcact ggcgggaata ctggaatgag cagagtgcaa     180

agcggagagt cccagccaca cccagactac cagccaggct catcaagagg gaatctggtt     240

accatgaaaa tggagtggtg aaggcagaga cggaacctc cccacggact aagaaactca     300

agtctcccta aggccaaagt gctaagaaca ggaatcctct tggtggggc cgagcanggg     360

gcaaggagcc caggccccct ccctgcctcc tccttcctgc ctgtgatgct ccgtctcaaa     420

cagccgaaac ctgtcttgca atgggggag gggngcgttt cnctttcctt cttcttggct     480

tcctcttatt cttccacaaa ccattctcaa                                     510


<210> SEQ ID NO 424
<211> LENGTH: 191
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

acattgtgcc tcaggatttt gataataatt ctggatattg gaacagaata gaaatgtact      60
```

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```
gtcgagagct gacagaaagg tttgaagatg tttgggtggt atctgggcct ttgaccttac     120

ctcagactag aggcgatgga aagaaaatag ttagttacca ggtgattggc gaggacaacg     180

tggcagtccc c                                                          191


<210> SEQ ID NO 425
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

gcggtgtgga ccgaggaaca acttggaaga tctacctgca acacaacatt tgtgtcactg      60

tacagttttg tggactgagc gaggaaaaac aacaaataat ttaagttggc tagagcttct     120

gtattttcaa agactgccac gtgccttagg aatactgttt tatctccata ctttggatga     180

cttgtt                                                                186


<210> SEQ ID NO 426
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

gttttggacc aacaagtgcc tcctttggtg aaggtgacac atcatgtgac ctcttcagtg      60

accactctac ggtgtcgggc cttgaactac tacccccaga acatcaccat gaagtggctg     120

aaggataagc agccaatgga tgccaaggag ttcgaaccta agacgtatt gcccaatggg      180

gatgggacct accagggctg ataaccttg gctgtacccc ctggggaaga gcagagatat      240

acgtgccagg tggagcaccc aggcctggat cagcccctca ttgtgatctg ggagccctca     300

ccgtctggca ccctagtcat tggagtcatc agtggaattg ctgttttgt cgtcatcttg      360

ttcattggaa ttttgttcat aatattaagg aagaggcagg gttcaagagg agccatgggg     420

cactacgtct tagctgaacg tgagtgacac gcagcctgca gactc                     465


<210> SEQ ID NO 427
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

tcctttgtgt agcattatca gcctcggtct ggcctctggc acctcaccct tgccatggct      60

gaccccaccc attccaaggc ggggtcacgg taccagcagc acttggggtg aggcctccaa     120

agcttcctca gaattgtggc tgtgccacgc tggaccacag ggtcccctc aagcatctcg      180

gggccctatt ctctctgagc acctggaggg ctggactcag gcttgtgcca gggcctgact     240

tgggcctggg ggccctagaa cactcctcct cctgagccta ctgccaaacg tcctcagtgt     300

tgtctgcacc tgctccgact ccttcagccg ccccattcag cgcccgctcc gtccagtgcc     360

cgccctgtgg ggccaaggcg gccgtgcctt actactctgt gtcttctgcc tcctctgagg     420

aatctggccc tgtctgacag tcccagaccc cccgttctct cctctttagt tgcatgagtt     480


<210> SEQ ID NO 428
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

ttcattcaca aacttccgct gtacctgcgt ctaaaaaggc ccaaacccga gagagacctg      60
```

```
atgccggagc cccctcactg ttcttctcca ggaagtggct ggggtcgggg aacagatgaa      120

tatttcatcc ggaagccgcc aagtgatttt ctcttcccca aacccaatag gttccagcct      180

gaactgtctg cccctgatct gcggcgattt atcgatggtc caaaccgggc tgtggccctg      240

cttccggagc tacgggaggt cgtctcctct atcagctaca tcgctcgaca gctgcaggaa      300

caggaggacc acgatgcgct gaaggaggac tggcagtttg tggccatggt agtggaccgc      360

ctcttcctgt ggactttcat catcttcacc agcgttggga ccctagtcat cttcctggac      420

gccacgtacc acttgccccc tccagacccc tttccttgaa gactggaggg ttgagaccag      480

gcccctgcc agttgaagtg agagagtttg gtgatactgt caagccctat cct             533
```

```
<210> SEQ ID NO 429
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429
```

```
gtgacctttc acgaacatgg gcatggctgc ggctccctcg tcatcaggtg catagcaagt       60

gaaagcaagt gttcacaacg gtgaaacttg agcgtcattt ttcttagtgt gccaagagtt      120

cgatgttagt gtttccattg tattttctta cagtgtgcca ttctgttaga tactatcctt      180

ataattgatg agcaagacat actgaatgca tatttcggtt tgtgtatcca tgcacctacg      240

tcagaaaaca agtattgtca ggtattctct ccatagaaca gcactatcct catctctccc      300

cagatgtgac tactgagggc agttctgagt gtttaatttc agactttttc ctctgcattt      360

acacacacac acacacacac acgcacacac acacaccaag taccagtata agcatctccc      420

atctgctttt cccattgcca tgcgtcctgg tcaagccccc ctcactctgt ttcctggtca      480

gcatgt                                                               486
```

```
<210> SEQ ID NO 430
<211> LENGTH: 97
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430
```

```
tattagttaa ttagtgattt cacagtatcc tttcgcaggc cgatccccac tccaaccgtt       60

ccctcagcaa ccccagggggt gtcagacggg gcaccct                               97
```

```
<210> SEQ ID NO 431
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (88)..(88)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 431
```

```
gctgcctttg cactggcgaa gggagggggca ctggttatgt tgtttccatt cgacagtcct       60

tccaaaggct ccctccagc gccactancc aaatccagaa aagcgtcctc ctccagaagg      120

taccaccaaa cctttaaaac ctttaaaggc tcctccagtg tcagattcaa atccaacatt      180

tctgcgcttt gctttcttta tggctctatt cttcaagact tcctcactgg ccatggagaa      240

t                                                                     241
```

```
<210> SEQ ID NO 432
```

-continued

```
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

tgagcctgtg cgtttttgcat actgggttgg tttgctgggg ctgcggtgac agcatatgcc      60

gcgagctggg ctttaacaga gatgtgtgct ctcacagctt tgcaggcggg ggtctgagat     120

cagggtgtcg cgggtggggg gtcactgctg aggccgtgag gggaatctgc tcaggcctgt     180

ccctggcttc tgggggctgc tggtggtatt ttcagttcct tggtgtgtgg atacttcgcc     240

ccatctctgc cttcacctgt gtcctccctg tgtgggtgct ggtgtccaaa atttcccctt     300

ttcgtagtga caccagctgt gttggattgg gcccaccct gctccagcat ggcctaatct     360

taactaatta catttgcaag gatcttatgt ccacaaaagt cacagtctga ggtgctgggg     420

gttaggactt caatatataa attttgcggt tacacaattc aatccatgac agaatccaaa     480

ggtttactct ggttataaaa acagtacaat aaaatattgt ttatagcctt ccctgta       537


<210> SEQ ID NO 433
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(56)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (109)..(109)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (186)..(186)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 433

gaaaacccgt tatgagacac aacttgaatt aaatgatgaa ctagaaaagc aaattnttta      60

tctcaaggag aaagtggaaa aaatccatgg aaactcttca gatagactnt cttctattcg     120

tgtctatgaa cgaatgccag tggaatcctt aaacacatta cttaaacagc tagaagaaga     180

aaagangact cttgaaaagtc aagtgaaata ctatgcactt aaactggaac aagaatcaaa     240

ggcttaccag aagatcaaca atgaacgccg tacataccta gctgaaatgt ctcagggttc     300

tggtttacat caagtttcta aaaggcaaca ggtggatcaa ctgcctagga tgcaa         355


<210> SEQ ID NO 434
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 434

ggcaagaagc caggtaaggc atgcagtctt tctgttcccc gttggggggag tggtattaag      60

gaactgtgtc ttcaggatac agtgagctgt aaaaatagac aacaagaaca cggaaactat     120

ggtagacgaa tgggctgagg acacagttca tgaaagagaa atatactcaa gatagaagaa     180

cctgcttcat cttagtggtg attttttgtaa aatgtaattt aaaatattcc ccgatgctgg     240

gagctaagta aaaaataaat aagtaaataa aatacaaaat tacatgtaca tttaaatgtt     300

ttttctctat caagtttat                                                  319


<210> SEQ ID NO 435
<211> LENGTH: 511
```

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 435

cacgatgacc ccagacatga gatccatcac taataatagc tcagatcctt tcctcaatgg      60

agggccatat cattcgaggg agcagagcac tgacagtggc ctgggggttag ggtgctacag     120

tgtccccaca actccggagg acttcctcag caatgtggat gagatggata caggagaaaa     180

cgcaggacaa acaccatga acatcaatcc ccaacagacc cgtttccctg atttccttga      240

ctgtcttcca ggaacaaacg ttgacttagg aactttggaa tctgaagacc tgatccccct     300

cttcaatgat gtagagtctg ctctgaacaa aagtgagccc tttctaacct ggctgtaatc     360

actaccattg taacttggat gtagccatga ccttacattt cctgggcctc ttggaaaaag     420

tgatggagca gagcaagtct gcaggtgcac cacttcccgc ctccatgact cgtgctccct     480

ccttttatg ttgccagttt aatcattgcc t                                      511


<210> SEQ ID NO 436
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)..(89)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (91)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(98)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 436

taagatccag ggttccagga ctgccaccaa ctcctgtcca gctgctctat ccagtgtccc      60

gattcagcaa tgtcaaatcc ctccagcanc nntgcnnntn ccggatacga cagctcgtca     120

ggatagatca catcccagat ctcccactgc ctaaacctct gatctcttat atccgaaagt     180

tctactacta tgatcctcag gaagaggtat acctgtctct aaaggaagcg cagctcattt     240

ccaaacagaa gcaagaggtg gaaccctcca cgtagcgagg ggctccctgc tggtcaccac     300

caagggcatt tggttgccaa gctccagctt tgaagaacca aattaagcta ccatgaaaag     360

aagaggaaaa gtgagggaac aggaaggttg ggattctctg tgcagagact ttggttcccc     420

acgcagccct ggggcttgga agaagcacat gaccgtactc tgcgtggggc tccacctcac     480

acccacccct gggcatctta ggactggagg ggctc                                 515


<210> SEQ ID NO 437
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 437

gctttgagga aaccactgtg caacttgaga tgtctgtggt tgtggggatg ttccatccct      60

ccgttcagtt gtgaagacct ctgctctgcc ctcagcaacc agagcctcgt cactctggac     120

ctgggtcaga atcccttggg gtctagtgga gtgaagatgc tgtttgaaac cttgacatgt     180
```

-continued

```
tccagtggca ccctccggac actcaggttg aaaatcgatg actttaatga tgaactcaat      240

aagctgctgg aagaaataga agaaaaaaac ccacaactga ttattgatac tgagaaacat      300

catccctggg cagaaaggcc ttcttctcat gacttcatga tctgaatccc cccgagtcat      360

tcattctcca tgaagtcatc gattttccag gtgttggtga actgcctgtg actcctctcc      420

tccccggccc ctacccctca gggataatga gttcattgct gggctagatg ttttagccat      480

gattctgcc                                                             489
```

```
<210> SEQ ID NO 438
<211> LENGTH: 580
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (275)..(275)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (284)..(285)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (293)..(294)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (303)..(304)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (313)..(314)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (322)..(323)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (327)..(327)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (332)..(333)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (350)..(351)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (369)..(370)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (386)..(386)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (389)..(389)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (408)..(408)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (427)..(427)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (446)..(446)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

<222> LOCATION: (523)..(523)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 438

agcgagaccc agactcgtac aacaaacacc tcttcgtgca cattgggcat gccaaccatt   60

cttacagtga cccattgctt gaatcagtgg acattcgtca gatttatgac aaatttcctg   120

aaaagaaagg tggcttaaag gaactgtttg gaaagggccc tcaaaatgcc ttcttcctcg   180

taaaattctg ggctgattta aactgcaata ttcaagatga tgctggggct ttttatggtg   240

taaccagtca gtacgagagt tctgaaaata tgacngtcac ctgnnccacc aanntttgct   300

ccnntgggaa gcnngtagta gnnaaantag anncggagta tgcaaggttn nagaatggcc   360

gatttgtann ccgaataaac cgctcnccna tgtgtgaata tatgatcnac ttcatccaca   420

agctcanaca cttaccagag aaatanatga tgaacagtgt tttggaaaac ttcacaattt   480

tattggtggt aacaaacagg gatacacaag aaactctact ctngcatggc ctgtgtgttt   540

gaagtttcaa atagtgaaca cggagcacaa catcatattt   580

<210> SEQ ID NO 439
<211> LENGTH: 581
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 439

gcacggacac ctatgaagac cagcagtgga gaccccccaa gcccactggt gaaacagctg   60

agtgaagtat ttgaaactga agactctaaa tcaaatcttc ccccagagcc tgttctgccc   120

ccagaggcac ctttatcttc tgaattggac ttgcctctgg gtacccagtt atctgttgag   180

gaacagatgc caccttggaa ccagactgag ttcccctcca aacaggtgtt ttccaaggag   240

gaagcaagac agcccacaga aacccctgtg gccagccaga gctccgacaa gccctcaagg   300

gaccctgaga ctcccagatc ttcaggttct atgcgcaata gatggaaacc aaacagcagc   360

aaggtactag ggagatcccc cctcaccatc ctgcaggatg acaactcccc tggcaccctg   420

acactacgac agggtaagcg gccttcaccc ctaagtgaaa atgttagtga actaaaggaa   480

ggagccattc ttggaactgg acgacttctg aaaactggag gacgagcatg ggagcaaggc   540

caggaccatg acaaggaaaa tcagcacttt cccttggtgg a   581

<210> SEQ ID NO 440
<211> LENGTH: 449
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 440

ggcgtataat tcagccctgt ttaaatatac ttgcctttca aattcttcaa gtaacatggg   60

aagtattctt gaaatgtcac attttctgcc ttccctctaa gtatgctttc tgaagaagtc   120

agggaaagtt agagtctgtg gcctgaggtg tctgctctgg gtggcgatag tgggcacctc   180

aggcaggtcg gtgacgttta gcacaggtgc cagggctcct gcctgctcct cctgtgttag   240

ctctgtgaag ttcatttagg aattttttt tcctatgcag tttaagaaat aatcctaatt   300

gtttttttctt attacctaag caatatattt ttattatagc aacctcagaa aagaaaaata   360

aaaggataat ttaaaaaact cattcatagt ctcagttacc cagataacct cggttgtcac   420

cttggagtat cttgttgtag tccctttac   449

<210> SEQ ID NO 441

```
<211> LENGTH: 457
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 441

agcagaggct catccgggag cagatacgcc aggagcgtga ccagaggttg agaggaaagg        60

cagaaaatac tgaaggccaa ggaacccca aactaaagct aaaatggaag tgcaagaagg       120

aggatgagtc aaaaggtggc tactccaaag acgtcctcct acggcttttg cagaagtatg       180

gtgaggttct caacctggtg ctttccagta agaagccagg cactgctgtg gtggagtttg       240

caaccgtcaa ggcagcggag ctggctgtcc agaatgaagt tggcctggtg gataaccctc       300

tgaagatttc ctggttggag ggacagcccc aggatgccgt gggccgcagc cactcaggac       360

tgtcaaaggg ctcagtgctg tcagagaggg actacgagag cctcgtcatg atgcgcatgc       420

gccaggcggc cgagcggcaa cagctgatcg cacggat                                457


<210> SEQ ID NO 442
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 442

aaggctatta acgacgcgat ttcacaaagt cggcagagtt ctgcgggaaa tcccctggaa        60

agactcaatt aaagagcagt gaagagagtg cagatcccgt cactggaagt tcggaaaatg       120

cagtgtcatc ttcagaactg atgtcccaga ctcccagtga agttctgggt accaacgaga       180

atgagaaact gagccctaca agtaatacct catatagttt agaaaaaatc tccagtctgg       240

cccctcctag catggagtac tgcgtttac tcttctgctg ttgtatttgt ggttttgaat       300

caaccagcaa agaaaacctc ttggatcata tgaaagagca cgagggtgaa attgtaaaca       360

tcatcctgaa taaggaccac aatacagctc taaacacaaa ttaggtggaa taatgactcg       420

agcaggaaag cagtagaaga ggattccttc accacagttt caccttacg ctgtcagaca       480

acttcctgcc acagaaga                                                     498


<210> SEQ ID NO 443
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (243)..(243)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (245)..(245)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (269)..(269)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (320)..(320)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (362)..(362)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

```
<222> LOCATION: (370)..(370)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (390)..(390)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (398)..(398)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (419)..(420)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (429)..(429)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (438)..(438)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 443

caaccgagag ggccggcagg agcttgaaat cattattgga gatgaacaca tttcttttac      60

aacatcaaaa atnggttccc ttattgatgt cagtcaatcc aaggatccag aaggcttatg     120

agtattttat tatcctgtcc aggaccctga agtgtttggt cttcagtctt actggattac     180

acttcaagat taaaccaatc taaactgaat attgatgtgg acatgggggg gtgggagtag     240

ttntnaatta ccattatcaa gaacatttng tgtcagggca gtatattttt ataaactata     300

tatgattatc tttaataaan tatgtgataa aatttaaaaa aagcaaaaca aaacttctag     360

anga ataccn tcaaaacctt ggtgagggan attcttanac agcacaaaaa tcattaggnn     420

aagatcaant ttaacatngt caaattaatc aatgacttct cttcctcaaa agacat        476


<210> SEQ ID NO 444
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 444

ttccagagct acccagacca tatggtgcac ccacagatcc agctgcagct ggtcctttag      60

gtccatgggg atccatgtct tctggacctt gggcgccagg aatgggaggg cagtatccta     120

cccctaatat gcc                                                        133


<210> SEQ ID NO 445
<211> LENGTH: 353
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 445

cgccgctgcg aattctcgga caaaactgtc aacagcccgg gcgcgccttt tggctctgcg      60

ggtccctcta tttatgcaaa gccgacctat gctacagccc cccaaccccc gacctggggt     120

agggaggaag agggtgccgg ggaagggagt ccgccctgtc caggcactag aggctccctt     180

gacgtttggc agatgaaaaa caactaagcc tttttgaggt gtagagattc tcaggtccag     240

gcgttaaaaa ataatggtca aaagaataat acaaaaatag taaaggtctt gaagaatgcc     300

agcgaagcaa ttcttttttta tttgaggaca cttgtctggt gtactttttc atg           353


<210> SEQ ID NO 446
<211> LENGTH: 416
<212> TYPE: DNA
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<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (275)..(278)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 446

gaggaagata tcctggctgg cactctttca gttgacagag agtgacctca ggctggggcg      60

gctcctcctc cgtgtggccc cggatcagca caccaggctg ctgcctttcg cttttttacag    120

tcttctctcc tacttccatg aagacgcggc catcagggaa gaggccttcc tgcatgttgc     180

tgtggacatg tacttgaagc tggtccagct cttcgtggct ggggatacaa gcacagtttc     240

acctccagct ggcaggagcc tggagctcaa gggtnnnnca gggcaacccc gtggaactga     300

taacaaaagc tcgtcttttt ctgctgcagt taatacctcg gtgcccgaaa aagagcttct     360

cacacgtggc agagctgctg gctgatcgtg gggactgcga cccagaggtg agcgcc         416


<210> SEQ ID NO 447
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 447

gctccccaca tgctggtggt gtactctgct aatggagaga tgtttaaact gagagctgct      60

gatgcaaaag agaaacaatt ctgggtgact cagcttcgag cttgtgccaa ataccacatg     120

gaaatgaatt ctaagagtgc tccaagctcc cgaagccgaa gtctcacttt gctcccacat     180

ggaacaccca attctgcgtc tccctgtagc cagagacacc tcagtgtggg ggcccccggt     240

gttgtcacaa tcacgcatca caagtcgcct gcagccgccc gaagagccaa gagtcagtat     300

tccggccagc ttcacgaagt cagagaggta cacactctcc tgcacgagga aagctgtttg     360

ctgcactggt ttactggata gattaactgg gttgaggctg tgtaattta                 409


<210> SEQ ID NO 448
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 448

gaggggcaca tgcaagtcac caaagtggga agccttcacc aaggccacac ccaaagtcta      60

ctgattgtct gtccaaagtt cgttgattcc tggccatgaa caagcacaat agaaaaagac     120

acagggtcct agtggctaca agtcaatgtg aattggcaca tggtctagca gttttaaaat     180

ctgacagtag agtatggcaa tgggcaaggg ccaagaagtc ctgagatggg aggtcagcgc     240

tctaactggg ctcagtggag gtctgtgacc agtgtctgga cactagctac aggggaccgg     300

gcagaggatt ctgggc                                                     316


<210> SEQ ID NO 449
<211> LENGTH: 473
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (241)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (341)..(341)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

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```
<222> LOCATION: (384)..(385)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (417)..(417)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (420)..(420)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (427)..(427)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (430)..(430)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 449

gcactttagt gattgctttt attacattag ttaagatgtc ttgagagacc atctcctatc        60

ttttatttca ttcatatcct ccgccctttt tgtcctagag tgagagtttg gaaggtgtcc       120

aaatttaatg tagacattat cttttggctc tgaagaagca aacatgacta gagacgcacc       180

ttgctgcagt gtccagaagc ggcctgtgcg ttcccttcag tactgcagcg ccacccagtg       240

naaggacact cttggctcgt ttgggctcaa ggcaccgcag cctgtcagcc aacattgcct       300

tgcatttgta ccttattgat cttttgcccat ggaagtctca nagatctttc gttggttgtt      360

tctctgagct ttgttactga aatnngcctc gtggggagca tcagagaagg ccaggangan       420

tggtgtnttn ccctagactc tgtaaccacc tctctgtctt tgtccttcct gag              473


<210> SEQ ID NO 450
<211> LENGTH: 512
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (363)..(363)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 450

gggaagtagg tgatgccagc cctcaagtct gtcttcagcc agggacttga gaagttatat        60

tgggcagtgg ctccaatctg tggaccagta tttcagcttt ccctgaagat caggcagggt       120

gccattcatt gtctttctct cctagccccc tcaggaaaga aggactatat ttgtactgta       180

ccctaggggt tctggaaggg aaaacatgga atcaggattc tatagactga taggccctat       240

ccacaagggc catgactggg aaaaggtatg ggagcagaag gagaattggg attttagggt       300

gcagctacgc tcaccctaaa cttttggtgg cctggggcat gtcttgaggc ccagactgtt       360

aancaggctc tgctggcctg tttactcgtc accacctctg cacctgctgt cttgagactc       420

catccagccc caggcacgcc acctgctcct gagcctccac tatctccctg tgacgggtga       480

acttcgtgta ctgtgtctcg ggtccatata tg                                     512


<210> SEQ ID NO 451
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 451

gtgaacattt caaccagcct tatagctgtt ctcatcatca ccttctgcat tgtgaccgtg        60

cttggaaggg aggctctcac caaaggggcg ctgtgggcag tctttctgct cgcagggtct       120
```

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```
gccctcctct gtgccgtggt cacgggcgtc atctggaggc agcccgagag caagaccaag      180

ctctcattta aggttccctt cctgccagtg ctccccatcc tgagcatctt cgtgaacgtc      240

tatctcatga tgcagctgga ccagggcacc tgggtccggt ttgctgtgtg gatgctgata      300

ggcttcatca tctactttgg ctatggcctg tggcacagcg aggaggcgtc cctggatgcc      360

gaccaagcaa ggactcctga cggcaacttg gaccagt                              397


<210> SEQ ID NO 452
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (32)..(32)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 452

gactgtaggt gcgtgggaga aactttgcag gntggg013gacc cggcggctgc tggccggtag       60

tgactggtgg gcgcgctcga ggactccaag gggcgcagcc cggggggcaga cccttgggtc      120

gggcggggat cttacgcttc ccttacccgc ccccttttgt ctttcacctc agccccgccg      180

gctgctgtgg gagcggcggc cgtccctctc ctggaggtcg tctcctggca tcctcggggc      240

cgcaggaagg aagaggaggc agcggccgga gccctggtgg gcggcctgag gtgagagccc      300

gaccggcccc tttgggaata tggcgaccgg tggctaccgg accagcagcg gcctcggcgg      360

cagcaccaca gacttcctgg aggagtggaa ggcgaaacgc gagaagatgc gcgccaagca      420

gaaccc                                                                426


<210> SEQ ID NO 453
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 453

ctaaagaaag tacacacact ctctcgctct ctctcggtct tataaaactc gttggtgtct       60

tataaaacaa acagtgataa tctcaagtta gaaaacagta ggtcctgaga accataagaa      120

aaatgactgg tgtgatgttg agtaacaagt tggtacagtt actttagcta tttattaact      180

tgctcatctc atagaacatt ttaatagatt tttcacacac ctcattatta aaaaaaaaca      240

aacatgctgg tgtcttggtt acccattatt cctctgtacc tgaattcagg ttggttttc      300

tatttggaaa agactttata aatgttggct taaaaagagg ttgagcacca gaatctcaga      360

atttaccacc aaagaactca tcca                                            384


<210> SEQ ID NO 454
<211> LENGTH: 407
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 454

agcataatga agcctgcatg tgcccagctt caataattac caatatcttg ccagttttgt       60

ttcgtttctc ctttgattct ctgtattgag caagtcttag acatcatacg tttcccgcgt      120

aagtacctta ttctacatca ttaaccagta aggacttttt aattaaccac aataccacta      180

tcacacctaa aatatagtaat tccttatgga tcttttcttt agacctattt ttgaaggcat      240

aaaagcagtt gagtttctgg agaatttttg gatggtgatt aatgacttga ctggctgctc      300

ttcccagagc tgtggcagct ctccccccgt agaagatggg gtttgtattg gcgcaccaag      360
```

atctccaaca gccagtgtgt gtttcccatt tcctgtaggt tccatca   407

<210> SEQ ID NO 455
<211> LENGTH: 223
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 455

tagtcagagt gacccatgta tctgggaaga ctctagtctg gactgtggcc cagcttgggg   60

accttgtgtg ctcagatcat cttcaggaag gaaaaggcat cctggagaca ggagtccatt   120

cactcctctg ctctctaccc actcatttgc ttgccaaact tagctttgcc agtgatagtc   180

aatattaaag tgtacttttt tcccctttaa tccaatatag ttg   223

<210> SEQ ID NO 456
<211> LENGTH: 160
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 456

tataattata accttaccgc atggacagtt ttgaatccta tgctaattgg ggtaattaag   60

tcaattattt catatgttat gttctcttca tgtgcatttt tcaatgatat attatgttcc   120

attgtgttgg aatgtgaatg ttcaattact tttccctata   160

<210> SEQ ID NO 457
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 457

ccacatccat ggcctaggag ctactgggca ggttcccggc cacacatctg gtgggctgtt   60

ttgttttttt ttttcctctt cccccagatg tcttgacggg atcactgggg ctctttgtga   120

gtgagggtgg ccaaactacc gccggaggag atggggtctc agagcgagag ctgcggaggg   180

ggaggggaag aagaaggcct cacttttgct gctgcggggc ccacacagcc gctgctactt   240

tggggggtgg ggaaggggcc aagctgcaga cacacacagt cattcatttc tgtccacacc   300

cctgtgggtg gcgggtgtgc gtgtgtgtgc ttgtgtgtgc gcacgtgtcg gcgctcacac   360

acacatgcta gcccactgat gcacccagcc cagggctggc agtctttgca gcgtggggcc   420

gtctcaccct ggagcctgga gaggatctat gcttgtttgt ttttg   465

<210> SEQ ID NO 458
<211> LENGTH: 212
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (158)..(158)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 458

gtgccgctgg cacccgggaa gacgctgggg gccggcgctg tagagccggg catgggctgg   60

gatgtgtttg gattccaatc cgggcctgac accagttcag tgacctcggg aagttcccca   120

ancctccggg cctgtttcct ccctctgaag tggcgacnag tagtagaacc gacctcgtag   180

```
gctcatcggg aggtcctgat gggagaaccc at                                    212


<210> SEQ ID NO 459
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (161)..(162)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 459

ggttgtactc aagatgtttt cctggaaaaa ttcattctgc tttctgacca ggatttccag     60

aaactctgac ccttctaaga ggtctgggtg gaattgtgat ggtgattctg ctagtagaca    120

gtgtaacttc tgcgtctaca aaagaggat aggccgtcac nnctcacatg gctttgcgtg     180

aaagcccaat ggtactgtct ctatggcaga gatgaggaag gaacaccagc gtcctccaac    240

tttcctgttc ttcctttggg ttaatggcca ctgtaaggaa acagttttct gccacgtgtg    300

gggtgatttg aatgtaaaat gcccaactct catagcaggc tg                      342


<210> SEQ ID NO 460
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 460

aaggggaaga tttgctgctg ctgccgggcc aagttcccgc tgttctcgtg gccgcccagc     60

tgtctcttct gcaagagagc cgtctgcact tcctgtagca taaagatgaa gatgccttct    120

aagaaatttg gacacatccc tgtctacaca ctgggctttg agagtcctca gagggtatca    180

gctgccaaaa ccgcgccaat ccagagaaga gacatctttc agtctctgca agggccacag    240

tggcagagcg tggaggaggc gttcccccac atctactccc acggctgtgt cctgaaggat    300

gtctgcagtg agtgcaccag ctttgtggca gacgtggtgc gttccagccg caagagcgtg    360

gacgtcctca acactacgcc acgacgcagt cgccagaccc aatccctcta catccctaac    420

accaggactc ttgacttcaa gtgacagccc caggtggcca ggcctccagg aggcaccagg    480

caggccctgt atcaggctag gacgctctga gctgtgcat                          519


<210> SEQ ID NO 461
<211> LENGTH: 208
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 461

tcccccctct gaattttact gatgaagaaa ctgaggccac agagctaaag tgactttttcc     60

caaggtcgcc cagcgaggac gtgggacttc tcagacgtca ggagagtgat gtgagggagc    120

tgtgtgacca tagaaagtga cgtgttaaaa accagcgctg ccctctttga aagccaggga    180

gcatcattca tttagcctgc tgagaaga                                      208


<210> SEQ ID NO 462
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 462

ctcagcattt agtgaaggta attccaaaat actggtatca gtactcttat ttataagtgt      60

acggaatgca taacatgaac attagtcaaa gaacttttaa tataattcac tttttaagtg    120
```

```
ttaaaatttta aaggtcaagt aaaattgtaa atttgtaata tggaaacatt aagcgtcatt      180

atcatacaaa ttattagcag ataaccttaa taaaaataaa cgtttgcggg ttttttttga      240

gacagggtct cgctttgtca cctaagctgg agtgcagtgc gcgatctcgg ctcactgcaa      300

cttccgcctc ctgggatcaa gtgattctcc tgccttagcc tcctgagtat ctgggtttac      360

aggtgtgtac cgccacaccc gtctctacta aaaatacaaa aaacaaaaaa agattagctg      420

ggcgtggtgg caggtgcctg tggtcccagc tgctcgggag gctgaggcag gagaatagca      480

tggacctggg aggcggagct tgcagtgagc tgaaatggtg ccactgcact cc             532
```

```
<210> SEQ ID NO 463
<211> LENGTH: 542
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 463

attatcgatc atgtctattg ctccccgtcc cttcgctgcg ttcagactgc acacaatatc       60

ttgaaaggtt tacaacaaga aaatcacttg aagatccgtg tagagcccgg cttatttgag      120

tggacaaaat gggttgctgg gagcacatta cctgcatgga tacctccatc agagttagct      180

gcagccaacc tgagtgttga tacaacctac agacctcaca ttccaatcag caaattagtt      240

gtttcagaat cctatgatac ttatatcagt agaagtttcc aagtaacaaa agaaataata      300

agtgaatgta aaagtaaagg aaataacatc ctgattgtgg cccacgcatc ttcccttgaa      360

gcgtgtacct gccaacttca gggcctgtca cctcagaact ccaaggactt cgtacaaatg      420

gtccgaaaga tcccatatct gggattttgt tcctgtgaag aattaggaga aactggaata      480

tggcagctga cagatccacc aatccttcct cttacccatg gaccaactgg gggcttcaac      540

tg                                                                    542
```

```
<210> SEQ ID NO 464
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (368)..(368)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 464

cagccccatg acagcgaagg gacctttctg tccccgcccc tgtccctgtg ctgggcccac       60

gtactcaccc acgtactggt gcccggctcc cctgggcacc cagagccccc cagataggcc      120

ggtggaggag gtggaggagc tgtcccccca aaactactgg cctgtggtct ggactccagg      180

gccccatttc tgatgtcgcc aggtgtgcct gagcccatcg gggccaggcc tgaggaagtg      240

tttcttggga ggatgggatg accccctgtt cccaagagat ggcagcacag tggaggccat      300

ggtggaaaag gccctgccat ggggtccttg agggccagga cagcctgagg gagggatggt      360

ggccactncc cacaaggggc ctggtgggaa cgggtcccag gacagactca tagctagacc      420

ccgttggcgg cctctgtgtt gaaccagaac t                                     451
```

```
<210> SEQ ID NO 465
<211> LENGTH: 467
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 465
```

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```
ggccccaggc agttttatga tgacacctgt gttgtcccag aaaaattcga tggagacatc        60

aaacaagagc caggaatgta tcgggaagga cccacatacc aacggcgagg atcacttcag       120

ctctggcagt ttttggtagc tcttctggat gacccggcaa attctcattt tattgcctgg       180

actggtcgag gcatggaatt taaactgatt gagcctgaag aggtggcccg acgttggggc       240

attcagaaaa acaggccagc tatgaactat gataaactta gccgttcact ccgctattac       300

tatgagaaag gaattatgca aaaggtggct ggagagagat atgtctacaa gtttgtgtgt       360

gatccagaag ccctttttctc catggccttt ccagataatc agcgtccact gctgaagaca       420

gacatggaac gtcacatcaa cgaggaggac acagtgcctc tttctca                     467
```

```
<210> SEQ ID NO 466
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (162)..(162)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (301)..(301)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 466
```

```
catacaccta ttaccataca ggggaagtcc ccaagctctc cggcctcaca gactctcacc        60

cacgggcaga gcattcttgg ctgattgagg ggaagttcca gcaatcagca caagtgttct       120

ttataccca  aatcactaaa acatatagag gggtctatgt cngtttcatc cataactcag       180

ccactggtgg aacaaatctc ataatcaaga ggatcatagt ccctggtaag tggatccctg       240

gagcattggc accatgtttt ccagtaaagt ctatctagct gtcagggaag agccacctgc       300

nctctgcaaa gggagaggga aaatcaaaac ccaggaaagg gaatatgttt ctgctccaaa       360

accaccagct tctgcctgtc cccttcactc tttctagatc attct                       405
```

```
<210> SEQ ID NO 467
<211> LENGTH: 110
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 467
```

```
gaaagagcga gagaaggggga aagacaagtc gggagaggcc ggtaggcgtg aggcgggcct        60

gaagcggcag cgggcggcct tcgtccggcg agagctaggc cgaggacccg                   110
```

```
<210> SEQ ID NO 468
<211> LENGTH: 204
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 468
```

```
ctgcccccca gggctagtga agtggcctct tggataccag ctcaggggac actggcccca        60

caggagttgt gagccctcta gggcagggtg ggagccggga ccctcaggtg tagctgagct       120

gtgacattgc tggtcatcct tggtgctctt gcttttttga aagatgcttt ttttttttt       180

aactgacgta gaatgaagaa ctgc                                              204
```

```
<210> SEQ ID NO 469
<211> LENGTH: 139
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

-continued

<400> SEQUENCE: 469

tcagatagga aggatggata tgtctttatc tacagcagaa gttagttacc ctttcatgag   60

gtgattagtt tacttctagg tggaaaaaga gaggactttg aacttggtgt tgtcacagga   120

gctgctctca tggacaaga   139

<210> SEQ ID NO 470
<211> LENGTH: 115
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 470

ctcagagatt actcagccag acagagatat tccactggtg cgaaagttac gttccattca   60

cagctttgag ctggaaaaac ntctgaccct ggagccaaag ccagacactg acaag   115

<210> SEQ ID NO 471
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 471

cagcgcctcc ggttataagt tgaagaaata agaccagttt ccaaataaat gacaaagagc   60

ttggtattcc tgcaggcatc agaatcacct ggaggaggag atgctgctgc tggtggtggc   120

ccagagacca cacattgaga accactgctc tagaaaacca tttgtctttg ctgatggaga   180

aacctggctc taatagaagg gcttgtatgt gtccaggaag tctagtgaat tcgaccatga   240

atccagacat ggccagtggc taaatcctgt gggaagacac tgtgcttctc tctgacccat   300

gaacactctg ctagtcaagc tctctgtcac aaagacaact tgaagagaca gagtggacct   360

cacagaagat accatcgtca ctcttaccaa tgcaactgtg gtgaacagga ccactattat   420

tccttagatc aaaaggacag cacattcaac agcatcctca tggcatgcca gcaat   475

<210> SEQ ID NO 472
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 472

cggcttgttg ggaccaccaa ccaaggggac cagcgcatcc tgcgcagcag cgcccctccc   60

tccctggctg ccctgctgt tagtcacaga ggccgcaagg ccaagacgtg agtgggctgc   120

ccctccacct aggctttcca ccgtggccac tccctccatg accaggcctg actctgttaa   180

ccactacttg aagtcttgag ggggaaagcc tccagggaga cataggggcc ttctcccttc   240

ttcccaccaa agtaggggt aggcaactgg ttgtcatgga aatgggggatc atcacagtcc   300

ccttcccctt caccccacgt ggctgggcag tgttaagggt ggcaagatag tctctgtccc   360

caccccttg tacttgattc cccagctgtc tttcacacag ccccccaccc ttaggggaag   420

ggggaggggc ttctctacaa tgaggt   446

<210> SEQ ID NO 473
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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```
<400> SEQUENCE: 473

gagacttggt ggtctgagct gtcccaagtc ctccggttct tcctcgggat tggcgggtcc      60

acttgccagg gctctggggg cagatttgtg gggacctcag cctgcaccct cttctcctct     120

ggcttccctc tctgaaatag ccgaactcca ggctgggctg agccaaagcc agagtggcca     180

cggcccaggg agggtgagct ggtgcctgct ttgacgggcc aggccctgga gggcagagac     240

aatcacgggc ggtcctgcac agattcccag gccagggctg ggtcacagga aggaaacaac     300

attttcttga aaggggaaac gtctcccaga tcgctccctt ggctttgagg ccgaagctgc     360

tgtgactgtg tccccttact gagcgcaagc cacagcctgt cttgtcaggt ggaccctgta     420

aatacatcct ttttctgcta acc                                             443


<210> SEQ ID NO 474
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 474

cctaattcac acaaagactc cttgtggact ggctgtgccc ctgatgcagc ctgtggctgg      60

agtggccaaa taggagggag actgtggtag gggcaggagg gcaacactgc tgtccacatg     120

acctccattt cccaaagtcc tctgctccag caactgccct tccaggtggg tgtgggacac     180

ctgggagaag gtctccaagg gagggtgcag ccctcttgcc cgcacccctc cctgcttgca     240

cacttcccca tctttgatcc ttctgagctc cacctctggt ggctcctcct aggaaaccag     300

ctcgtgggct gggaatgggg gagagaaggg aaaagatccc caagaccccc tggggtggga     360

tctgagctcc cacctccctt cccacctact gcactttccc ccttcccgcc ttccaaaacc     420

tgcttccttc agtttgtaaa gtcggtgatt atatttttgg gggct                     465


<210> SEQ ID NO 475
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 475

agaatgcaaa gaggccgctt ccctaagagg cttggaggag ctgggctcta tcccacaccc      60

acccccaccc caccccacc cagcctccag aagctggaac catttctccc gcaggcctga     120

gttcctaagg aaaccaccct accggggtgg aagggagggt cagggaagaa acccactctt     180

gctctacgag gagcaagtgc ctgcccccctc ccagcagcca gccctgccaa agttgcatta     240

tctttggcca aggctgggcc tgacggttat gatttcagcc ctgggcctgc aggagaggct     300

gagaccagcc cacccagcca gtggtcgagc actgccccgc cgccaaagtc tgcagaatgt     360

gagatgaggt tctcaaggtc acaggcccca gtcccagcct gggggctggc agaggccccc     420

atatactctg ctacagctcc tat                                             443


<210> SEQ ID NO 476
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 476

gactcagtgg gcactagaac gcctgaggct gcagctgggc tccccggggt ccttgcagag      60

gaaactcagt ctgctggagc aggaatccca gcagcaggag ctgcagatcc agggcttcga     120

gagtgacctc gccgagatcc gcgccgacaa acagaacctg gaggccattc tgcacagcct     180
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gcccgagaac tgtgccagct ggcagtgagg gctgcccaga tccccggcac acactccccc      240

acctgctgtt tacatgaccc agggggtgca cactaccccca caggtgtgcc catacagaca      300

ttccccggag ccggctgctg tgaactcgac cccgtgtgga tagtcacact ccctgccgat      360

tctgtctgtg gcttcttccc tgccagcagg actgagtgtg cgtacccagt tcacctggac      420

atgagtgcac actctcaccc ctgcacatgc ataaacgg                             458


<210> SEQ ID NO 477
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (342)..(342)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 477

agcatcctga accagctgtg ttttattatg cacagatatc gtaaaaattt gactgccgca       60

aagaaaaatg agttggtaca aaagacaaaa tcagagttca atttcagcag caagacttat      120

caagaattta attactattt gacatcaatg gttggttgcc tgtggacgtc caaacccttt      180

gcgaaaggaa tatatattga ccctgaaatc ctagaaaaaa ctggagtggc tgaatataaa      240

aacagtttaa atgtagtcca tcatccttct ttcttgagtt acgctgtttc cttttttgcta      300

caggaaagcc cagaagaaag gacagtaaac gtgagctcta tncggggaaa gaaatggagc      360

tggtatttgg actatttatt ttcacagggg ttacaaggct tgaaacttttt tataagaagt      420

agtgttcatc attcttccat tcccagagca gagggcataa actgcaacaa tcaat           475


<210> SEQ ID NO 478
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 478

ctcgcagagt tccgtcgatc aggactggag gaagccacgt ttcaacagat atatagtcaa       60

catgtggcac tgtgcagaat ggagggactg ccgtacccca ccatgtcaga gaccatggcc      120

gtgtgttctc acctgggctc ctgtcgcctc ctgcttgtgg agcccagcag gaacgatctg      180

ctccttcggg tgcggctcaa cgtcagccag gatgatgtgc tgtatgcgct gaaagacgag      240

taaaggggct tcacaagtta aaagactggg gtcttgctgg gttttgtttt ttgagacagg      300

gtcttgctct gtcgcccagg ctggagtgca gtggcacgat catggctcac tgcagccttg      360

acttctcagg cttaggtgac cccccaacct catcctccca ggtggctgaa actacaggca      420

catgccacca tgcccagctg atttttttgta gagacagggc ttcaccatgt tgccaagcta      480

gtctacaaag                                                            490


<210> SEQ ID NO 479
<211> LENGTH: 460
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(77)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (364)..(364)
<223> OTHER INFORMATION: n is a, c, g, t or u
```

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<400> SEQUENCE: 479

ttttttaggg actctcaacc tcctggcagg gttaaaggga gagtacttta aacccatata      60

ccagctgtgc tnnnnnntct ctcactttgc cctgggtaag ctgctgtagg gtcagaagta     120

accctttctg tgccagttga gaatgagcct gtgtggtagc tgatgtcaga ggacaaagct     180

ctctgcaagg gctggacaca gagctgcaga gtcctgaaca tccctccttt caggctgcag     240

aagggagagg caatgaagac aggtgctccg gaagcagcat cagggctctt ggaggggact     300

ggtggggact caggctgggt gcagcctcca aacagagaac ggaacttagg tgtgtctcta     360

cagnctaggc ccagcctagc ccagcccaga acaaacaccc ttcagagcct aaccaaagaa     420

cataagctgc aaaatgtgca cccatatttt aagctgcttt                          460


<210> SEQ ID NO 480
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (77)..(77)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 480

cctgtctcct acatttagcc aatgaaaaga atctaaaact ggaaggaaca gaggacctct      60

ctgatgttct tgtgagncaa ggagattgag ttcactatgg agaagtcagc agcaggaggc     120

ccatccctta ctcagttgcc gggacatccc cagtctcggg ggaagaagat gccatgggct     180

tatacccagg ctgtagccaa ctaccaacgt gcctgtttgt ttgttgctct ttccttctct     240

ccatcatagt ctgggtgcca gcgccctgaa gctccgtgct caactgatta aactttactg     300

ccctatggtg accatctagg agaggggagg gcagagggag tgagggtact attctggatt     360

gagaaaacct atatccattc tttatatcaa tgtatagttt tagtctccta aattgatctg     420

ttattttcca aactattctc ttgtagaaaa ttttccagtg ggcacttaat ggtgcccttg     480

aagaacttcc ta                                                        492


<210> SEQ ID NO 481
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (197)..(197)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (247)..(247)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 481

ggagggagag gtccctgcaa ggtcccttcc cgggcagggg agggatggaa atgccgtcac      60

agtagtaggg actggagcgt ctacaaggat ggagggagc tactcaggcc taacgttagc     120

tacaaggaaa aaggacgcct tccgtgacag atccttgagg tgtctgtgtc tgccccaagt     180

ggccggcagt ggccttncct ccgggcccaa ggcctgcagc cacctgctct aactcttgag     240

tgggggngcg ggggggacc tgcagggct cggggacagg acagcagcaa gaggcagggg      300

ccgaggacgg aggccttccc gacagtgggg tgggttgtac attcaagtgt gaggtgaacc     360

ctttggtggg gaggggcccc ctgaagcctc ggcggggcca cccctccccg cggcgcctct     420

gagtctaggg agagggctg ctggctcggc ccggccggcc tggcttcaca gagggtctgc      480
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ggattgacac tggttctttt c   501

<210> SEQ ID NO 482
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (185)..(185)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (271)..(271)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (306)..(306)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (313)..(313)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (352)..(354)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (357)..(357)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (359)..(359)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (361)..(362)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (365)..(365)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (367)..(367)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (371)..(371)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (373)..(374)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (376)..(377)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 482

gtgaggagct gttttcatct gtgtctgttg gagatcaaga tgattgctat tccctgttag   60

atgatcagga cttcacttct tttgatttat ttcctgaggg gagtgtctgc agtgatgtcn   120

cntcttctat tagcacttac tgggattggt cagatagcga gtttgaatgg cagttaccag   180

gcagntgaca ttgccagtgg gagtgatgta ctttctgatg tcatacccag tattccaagt   240

```
tcaccttgcc tgcttcctaa aaagaaaaac nagcaccgga atttagatga actcccttgg      300

agtgcnatga canatgatga gcaggtggaa tatattgagt atctgagtcg gnnngtnant      360

nntgngntgg ncnncnntac tgtcctgtgg tctagtgggc agggacctgg gggccatcag      420

tggctgtagg acttttttac ccctctgttc ctggcctaaa tatgtgatgg gtatgcttca      480

ccttaagtgg                                                             490


<210> SEQ ID NO 483
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 483

ctttcacact gtggcagccc agtgaagcag actgggccat gaactctcct agccctgggg       60

ccnagcctgt tccacaggca cccctgcagg aggcgctgcc aggagagcct tccatctcgg      120

ggctctttga ggttccctcc ttctgggtgt tcttcaggct gagcagagag gctcctgtac      180

cctctctctc ggaatctgaa gagccagatt taggccgggc aaaggggctc a              231


<210> SEQ ID NO 484
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 484

ggtgctggaa aaactactat cttgtttaag ttaaacagg atgaattcat gcagcccatt       60

ccaacaattg gttttaacgt ggaaactgta gaatataaaa atctaaaatt cactatttgg      120

gatgtaggtg gaaaacacaa attaagacca ttgtggaaac attattacct caatactcaa      180

gctgttgtgt ttgttgtaga tagcagtcat agagacagaa ttagtgaagc acacagcgaa      240

cttgcaaagt tgttaacgga aaaagaactc cgagatgctc tgctcctgat ttttgctaac      300

aaacaggatg ttgctggagc actgtcagta gaagaaatca ctgaactact cagtctccat      360

aaattatgct gtggccgtag ctggtatatt cagggctgtg atgctcgaag tgtt           414


<210> SEQ ID NO 485
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 485

tcctctgtcc tctatattca gcatgttcct tgtcagctgc tgggccggcc ctgccttgcg       60

ctagcagagc ctctcctggc agcttctcag gtctccctaa tggagacacc aggctactag      120

gacactggct ggggccaccc cctcctgcct aatgcctcac cttacagctg gggaaactga      180

ggcctggaat ggcccagagt caccaaggca aagttggggc tggtcccagc ctgaggctcc      240

agctgatgcc ctcagctccc agagagggggg tgccccatct agctgggtgc aggggtcact      300

gcttgtcagc tcagggccct gtgcccgctt gcctgttccc ctacatctgt gcctgcacat      360

ccagaactgc ctccttgccg ctgcctccag gaagcccacc ttgagccaga gtcaagggct      420

gcagcactgc ccgatagaac acgcccgccc tcactgctgt tcttgcctta cagccaccat      480

gggaaagctg caacctttct gttttatt                                         508
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<210> SEQ ID NO 486
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (400)..(401)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (410)..(410)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 486

tgtcaacttg tcatatacac ctccagggac caaaaacaaa agcagctcgg agtctgtgtt      60

gcctgattgg aaagtagaag ctctggtgta tgctacagca cataacacat ttttactaaa     120

ggaaaaaagc taattatgtc catgcctctc gtaaaactgg ggggaacctt aaagagaaag     180

aactaaggct taagttatct gtagtataat caattagaag taatgaatgg atgcatgtaa     240

aatggatgtg attttttttc aagcttattt tgaaatctta aaaatcaggt tacaccatag     300

ctactcaaaa gttttacaca cttaaaactc agatcagtaa gtgttggtac cttttagact     360

cataaaattg aataaaccat tgcaatgctt taaaaaaaan naaaaaaaan ggttttattg     420

ctatgatttt atggcagaca catccaagca aaaccatttt ccaaatgcag accttcctga     480

tgttatctga aatctgataa aatgacccta ctctctgctg tggttcattc ttgctccatg     540

ctgtccatat ttatg                                                       555


<210> SEQ ID NO 487
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 487

gtggcactta ggcactatat tattgatatc tacaatggcc tcctggatgc acaaaagacc      60

ctgaagggct tttttgatca gcaaaacaaa aacagaaaag caaaaaacag ttaatttttg     120

tttggtcaag tttactcaac cagaccacct tgataccaac aatgctggag agcatttggc     180

aagagcaggg ccacaatgcc aaattccttg gaaaggtaga cttcctatga tactttcatg     240

gattggcaaa tttgtggggt ttttttggta gtagcttttg agaatgttag tttctggctg     300

gggtagtgac ttacatctgt aatcccagca cttcgggagg cgaaggcagg tggattgctt     360

gtgcccagga gtttgagacc agcctgggta acatggtgag accccatctc tattttttata     420

aaattaaaaa aaaaaaaaaa gatagagaat gttactttcc tataaagcca tgatacccta     480

agtactaaga catgtctgtt gttgtccttt ccttcataac atttctcata acccgtaatt     540

t                                                                       541


<210> SEQ ID NO 488
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (106)..(106)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (140)..(140)
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<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 488

cagccctgac gtgaactcat tttattttgg ccaggaccca gaaaggagtc tactgctaag   60

atttcagcat gtcctgtggc tgagtnaatc agagttatga caggganggta ccgggcacac   120

catcgcaatg ctccatcaan gctagtatgt tgtgttcttt ccttcatatc aagtcaactc   180

aagcttgctc tacttacctg gtgtacacag tctaagaact gtaagaagac tggagcaaaa   240

ccactcccct gacagttgag ggtcaagctg ctcctctgac tgaatttgtg accaaaagag   300

agccactctt tttcaaccaa catctggaag ccttcaagtg tcctataaaa gggatcactg   360

agtaactgaa ccagggatgt cacctagggc ataagcagga tggattgtca ttaattttag   420

ttctgaaaaa ggcctattac taagataaaa gcacttcctt ctgatgatag ctaattcaca   480

aatttacctg gacagcaaat ttgttcacta accattccag gat   523

<210> SEQ ID NO 489
<211> LENGTH: 306
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 489

cggctgtacg actccataat gggcatgggg actcaagata aggtcctgat cagaatcatg   60

gtctcccaca atgaagtgga catgttgaaa attaggtctg aattcaagag aaagtatagc   120

aagtccctgt actactatat ccagcaagac actaagggtg ctgtacctgt gtggtggaga   180

tggctgaagt ccgacacagc acgagcgtcc agaaatggtc ctccccatgc ttccagctaa   240

caggtctaga aaacccgctt gtgactagca gtccctgtgg ctgttcctgt gaggatgacg   300

ttagca   306

<210> SEQ ID NO 490
<211> LENGTH: 170
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 490

agaagattcc cttgaagcct tctccttcca aaaagtttcg gtctggctca tctttctctc   60

ggcgagcagg ctccagtggc aactcctgca ttacttacca gccatcggtc tctgggggaac   120

acaaggcaca agtgacaaca aaggcagaag tggagccagg cgttcacctt   170

<210> SEQ ID NO 491
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 491

tgggggtgac tgctgcttat taagatgatt catttcattt ccactcgtgg ttgtgatttt   60

caccttctca aaactgagtc agcaagagaa aatcttgtct tagaagggcc agataacact   120

tcgctgtgag aacaggaggg ataatggatt ggagatggct atgtgtaaag cagccctgcc   180

tgctgattta acacactttc aaaatagatg tgtcagtatt catttaaagc aagactctga   240

tgacagaagg aaccttgaaa actacctgat attgaaatgg ttgtgccctt tatagccctt   300

ttgcatctcc ttgactttcc agtcatgcct cctaaatcag aagaaaagct gcaaagaaaa   360

tgttttgtgt ggttctgggc ttatttgaat aatgttcatg accacaggct gccatagcac   420

aagtgagaat ttcagaccac aagggtttaa ggagcagtgc tctcttctct caaagctcag   480

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aacggtctct ggatccatgg tatcgtacac ccagtgtgga tattaacatt ct                532


<210> SEQ ID NO 492
<211> LENGTH: 559
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (232)..(232)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (259)..(259)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 492

aagggaagtt agcaccttcc tcttggaggt gctgaggatt aaatgagata atacgtggaa         60

agcattaggc atgtagcaca gttagcagat ggtggttggc tccctctgct tttccatcag        120

tctgtggcct agtttaaatg gtgggaggaa gggtgtgaga tttaaggctg gttgtaaggg        180

atcagtcagt gtagttggaa aaattgtaag atgaagttat aggatataga cncaaacctt        240

cctggaaggc cagaaagtnt gcatagcttc aataaaggat ttggctgaaa gcagcgtaat        300

cccctttacc ttgagttgat agcaatagag caaataacat gggaacgtgg gggagtttat        360

tgaatagctt gtttactcat gtggtcctaa gaccaacctt tgattatcca cgggtgcatg        420

attgctctct actcggtggt cggcaaattt aattacccac aggtgtgttg actcaaagcc        480

tctgtcatta aatctatgct gaataaatgc cgtcaggcca gctagtcaag gtgcacaact        540

cttttgtgc gtggtgtgg                                                     559


<210> SEQ ID NO 493
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 493

gtaagtctca gtcctttaaa actcagaaaa aggtgtgttt tccaaattta atatttcctt         60

tctgtaagtc tcagtgtctg cactatttgt cttggagact taaaattatc ccttgaaagc        120

ataagaagta caccccaaac cagctttgtc cttcctgtcc tcttctagtt tacattttat        180

gtggttagta attttgtacc taaaagtatt tgaaattcta taaatttgga cttgacgtga        240

gcaaaagaaa atttctacgt aagcgaaact aataaaacta cagtcac                     287


<210> SEQ ID NO 494
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 494

ctgtggcatc tataacctga gttcagtcac ttaataccga ggtcctgcgc tctgctgtgt         60

gcctggccct gggctgggca ctggggacat agcagtgacc gagacagaca ggctcacaag        120

gagacatacg acaaccaggt aaacatggca gacaagagca tgtcagatgc gctgtgaaga        180

acactgcggg gcccctccta ggaggtggca tgagttacat gcagacagag acgatccggg        240

ggcagacgga gttccatgtg gggcagtggt gagggcagac gctctggggc tgggatccct        300

gggagtgttc gagaagcacc gagaaggctt ctgtggctgg agccggccag ctgggggaga        360

tggggccagg gagatggcag gggcctctcc ctgtcccagg acccagagcc aagggaggct        420
```

ttaagcccag gaccaggggt ctgaaaacga aaagcactca cagtccttga acattg   476

<210> SEQ ID NO 495
<211> LENGTH: 542
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 495

ggcaacctcc tggacaagga cgacctggcc atcccacccc ccgattacgg cgccgcctcc   60

cgggccttcc ccgcccagac ggccagcggc ttcaagcaga ggccctacag tgtggccgtg   120

cccgccttct cccagggcct ggatgactat ggagcgcggt ccatgagcag tggcagcggc   180

acgctggtgt ccacagtgtg aggacgctga ccccgggcag ccgctgctct gaagagcttc   240

cgcgccttcc ccctggtctc gtccgttttc ctcctcagct ctcgctggtt tgttcttggg   300

ttgttttttct tttccacctg ccccatgcct tttggttggt gaccccagac tctgtgatcc   360

cccagggtcc atggtgctgc tccatccgcc cccctcccc tgtgtttacg cgccccatcc   420

tgtgtgtccc agccttttga gcagaaactg ccaggcagga cctgctgggc cgtgcggggc   480

accctcggcc tcaccctgca gtgtctgtgg cactcactgc ttttctaagg ctcgccgtga   540

gc   542

<210> SEQ ID NO 496
<211> LENGTH: 438
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 496

gagaggtatt atcgagacat tgcaaagatg gcatccatca gcgaccagga catggatgcc   60

tacctggtgg agcagtcccg cctccacgcc agcgacttca gcgtcctgag tgcgctcaac   120

gagctgtatt tctatgtcac caagtaccgc caggagattc tcacggctct ggaccgagat   180

gcctcttgtc ggaagcataa gttgcggcag aaactggaac agatcatcag cctcgtgtcc   240

agcgacagct aaggtggtgg aatcggtgag gaggggggctt ctcagtcctg tgccgtcctc   300

ccatccaggg gagtggctgg ctcaagcctg ggtccccggg ctgagccctg gattgggtat   360

cgtggggcag gtcaccctgg ccacgatgcc cccggcacac ccaggccccc ttcattagtg   420

ccttgctttg ggccctgc   438

<210> SEQ ID NO 497
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (248)..(251)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 497

taagttctca tccaacattt ctcctggcca tccattctcc atctttaaag gcaatcacca   60

ttgccagttt cttctgtatc cttctggaaa tacaatatat tacataaatg acagcattct   120

atattctctc ttctatatct tacctatttc tgtgaataat ttattttgga cagcattttta   180

tgtatgaata ttcacaaatg tgcttcctta tttcagaggc tgaactaata aaaattttgt   240

ttattttnnn nttgaggcaa tatttttata tggtaccta atctttaata cttaacctgc   300

cagactttaa ccgtaacaca ataatgtatt gccaaatagc accattcttc ttctctcact   360

ctcttgccat gggggctctt aaaaaaaaaa gtatacatct aaggtgtaca acatgctgt   419

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<210> SEQ ID NO 498
<211> LENGTH: 477
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 498

accagtttac ctaggccttg gactgccaaa tagctacaca actgcttaag ctggcctata      60

aggacagacc agagacaaag caagaagatc attggtccag actgagaaga aagttgccag     120

agggatgtct ccactaaggc ctttgagcag ggattaatgc tgtcaccacc ttggtggaga     180

acaagaaagc tcagctggtg gtgactgcac gtgacaatgg atctcataga gctagctgtc     240

ttcctgcctg ccctgcatca taaaatacaa agggaagaga agactgggat gtctagtcca     300

caggaagact tgcaccactg tcgccttcac acagattaac ttggcagaca aaggagcttt     360

ggctaagctg gtggaagcca tcagaaccaa tgacaatgac agacaggatg agatccactg     420

tcactaggga ggcaatatcc tgggtccaaa atctctggct ctcattgcca agctgga       477


<210> SEQ ID NO 499
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 499

tgagggaggg atgtgcctct ggccacgtgg ttaccttgca gtgcacagcc tgtggtcata      60

gaaggggcta cagctcacgc atcgtgggtg gaaacatgtc cttgctctcg cagtggccct     120

ggcaggccag ccttcagttc cagggctacc acctgtgcgg gggctctgtc atcacgcccc     180

tgtggatcat cactgctgca cactgtgttt atgacttgta cctccccaag tcatggacca     240

tccaggtggg tctagtttcc ctgttggaca atccagcccc atcccacttg gtggagaaga     300

ttgtctacca cagcaagtac aagccaaaga ggctgggcaa tgacatcgcc cttatgaagc     360

tggccg                                                               366


<210> SEQ ID NO 500
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (193)..(193)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (210)..(210)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (379)..(379)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (443)..(444)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (446)..(446)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (448)..(451)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 500
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```
gaacaatcgt cttttgaact tccagtaggc ccacagttgt tggttgttcc tcaaaacagg      60

ttgtggctcc tgttgaataa gatgatccat taaaaactga acaaggttga ggagaaatag     120

tgcttacgtt gaaaaatctt taagtctttg tccccgttct ctaacttcct tacgttttcg     180

tttatttagc tcnatcccca ctatctactn gaatttctca tatttaaacc aagatgggag     240

actaggtcat taggaaaata ttaccgtcta caattttctt atactttgat ctgtctttta     300

tttgattgta agttgctgat ggacagtgat cattagaaac tgaattttgt ataatactag     360

ttttatatga aactagatnt ttattgcgct caggttatgt tccttttacc tccttcctta     420

ataaagagac cacttgaaat aannanannn nttccaagta ctgtctgcac cttatcccac     480

ctctttccca tttatgagat agtgcaaaac cctagcacag tcttttccat ttagtaa       537
```

```
<210> SEQ ID NO 501
<211> LENGTH: 332
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 501

aagtatctcc atacaaaata cggttgaatt acaaaaagaa aattgtaaca ttagcatgga      60

caaacctggc aggtactcct taactctcct aagtaataaa aactgtaaaa tgcaaataag     120

ccttcgatga catttactaa cctttactaa agtatcaatg atgacttggt tgtttaaaca     180

gctgacattt gggcaatttg agtatgtcaa actcaataat actggttttc atttgcaaga     240

tccacttaaa acttaaggag gccaaaaaac atcatttaaa ataccctata aattataatc     300

atacatatga tacgaaaaat atcctacttc ag                                  332
```

```
<210> SEQ ID NO 502
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 502

agggtaactt ccagtgtcac aatgagcagt tctgtaagtg ggtgcctctc agcacatttc      60

tatgaatata ttatgtagat aggctgtatt gattttggta gcattgacac cttcttaggc     120

aattagttga agaaaactgc aaaatatttt cttatgtaat agctgtatag agcaatagca     180

atcaaagcat gagaaggcac taacgctggg atgaaagatg agattcagag gtgactgaga     240

atcatgtgag tgatggctgt atattttgtg taaaatatat gtgtgaaaat gaactaagag     300

tgagttactc agcactctca agaattatgc agattctgca ttttttcttat gccgtgtgcc     360

taaaaaccta cttga                                                     375
```

```
<210> SEQ ID NO 503
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 503

gggacaggat gaccttcccg aggaactcan tggcctgggg tagtttaaga agtaatgttc      60

tttctttctt tctcttttcc ctacctcctg ctaacccaac cagagatccc cttccttgct     120

gagagggttg ggggcaggag gagatttggc agtgcctgca ggttgcctgg ccaggtggag     180

aggggggaaag aggaagggca ccgtgggtgt aagatgcctt tctcctccac ccatcgaaac     240
```

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cagccacccc ttccctgtgc caccaagaca gccttttcca gtggccatcc taaggggaac    300

tcccaaatgg gtgttgctgg tggacacaga tgctcccccc aatggaagcc ccaagctctg    360

aggtatgcgg gtagaggctt tggataggtt ttcttctgct cccctctttt atagatctag    420

gctgcttggc tgcctgtctt tctaggcagt cccccctagag gaaaaatg    468


<210> SEQ ID NO 504
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 504

accccaccac gtaccagatg gatgtgaacc ccgagggcaa atacagcttt ggtgccacct    60

gcgtgaagaa gtgtccccgt aattatgtgg tgacagatca cggctcgtgc gtccgagcct    120

gtggggccga cagctatgag atggaggaag acggcgtccg caagtgtaag aagtgcgaag    180

ggccttgccg caaagtgtgt aacggaatag gtattggtga atttaaagac tcactctcca    240

taaatgctac gaatattaaa cacttcaaaa actgcacctc catcagtggc gatctccaca    300

tcctgccggt ggcatttagg ggtgactcct tcacacatac tcctcctctg gatccacagg    360

aactggatat tctgaaaacc gtaaaggaaa tcacaggttt gagctgaatt atcacatgaa    420

tataaatggg aaatcagtgt tttagagaga gaacttttcg acatatttcc tgttcccttg    480

gaat    484


<210> SEQ ID NO 505
<211> LENGTH: 277
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 505

ctgcacagtc tccagtgtgg aaagctgtgg gaaaggaagg agcaggttct aggtcttcag    60

gattttctgc atcttaaagc agctcatctc ctttgccctc ctagggagca gggggggccta    120

gctttgggat cgtccnccta gcctcagaaa taattgttca agaaataaca tttctcacac    180

aaaggataaa tgtttgaggg gatggatacc ccatcttcca tgatttgatt attacacatt    240

gcatgcctgt atcaaaaatc tcatatatac acctact    277


<210> SEQ ID NO 506
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (380)..(380)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 506

gggggtgatt agtatgttgg gacaaacacg ctgttgctaa atggaaacac tgacctcaca    60

gtgcatcctc ctgccaacac acacacacac acacctctca cacatgcacg cttacacaca    120

cacacacaca cacacacaca cacacacata cacacacaca cacacgct ctctctctct    180

ctctctctct ctctctgtca gtgtgttatc ggtgtggagc ggaggccgcg gaggctcctc    240

ggtccttcag caccccctcgg cccgacgcac ccacgcccct cacccccga gagccgaacg    300
```

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```
ctccccgcac cgcccccggt cccttccctc ggccgggagc gacttctgca gctcgttctt    360

ccgaatcgca ccagcaatgn cggccagccg tagaggagg aagagcccgg ggagcccgag     420

catagcgtaa acggctctct gaccttaatt tcatcctgca tggcgaatct ctgccgtctc    480

tctgaacgca gaagggtctg agactggccg tctcc                              515


<210> SEQ ID NO 507
<211> LENGTH: 259
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 507

ttcagtttat actcaaagcc ctgcagtttc ctgacagcac agagcacacc tgtcacgcga     60

gcaggatgaa gcccagaggc tgcctggtga agtgggcggc gcgctggaaa atccacgtag    120

ctttgttccc tccacgggga gcgtgcaagg ccctctcgag cactacggga gcctcgcctt    180

ctgcacagac ttcggagcca ggtgctggag cggcagcaac tgaggggcgt ggatgtcttt    240

gcatggttcc catacgttt                                                 259


<210> SEQ ID NO 508
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (189)..(189)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 508

atagcagtgg actgtcactc atcagtatct gcagttctgt ttaccaaagc ctgcttgcta     60

gagacgtttc agggcctcct tccctcaaag cgtccactgt acctccatct ggatacaatt    120

agctggctcc ccacttcctg gactgacggt aaccaccttt tccaatgacc ctgaagaaaa    180

catgcaatnt aagctgcttt aagagtaacc tacaactgag gacaaatttt ctatcaactc    240

ccagtacccc tctctgccgt ggctgatttg ttactggttt tcctt                   285


<210> SEQ ID NO 509
<211> LENGTH: 274
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 509

gaggtgcatg ggatcaatgg gacccaatgg ggccagactc tgaggatggg atggtagtag     60

tgaaggacat aggatggggg tagagtgtgg agactttttg aaatagtata gatgaatgcc    120

ctgaggggac tgtgaacaag ctctgcccct cttaggaaat caatgggaa tcaactaaat     180

taaataaaaa atggggtcaa gattaagagg cagggtcacc cagggaatgg tttaggtcct    240

ggcaactctg aaggggttgg aagggctggc agga                               274


<210> SEQ ID NO 510
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 510

gcgtgggttt ttgtatccag agctgtttgg atacagctgc tttgagctac aggacaaagg     60

ctgacagact cactgggaag ctcccacccc actcagggga ccccactccc ctcacacacc    120

cccccccaca aggaaccctc aggccaccct ccacgaggtg tgactaacta tgcaataatc    180
```

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```
caccccaggt gcagccccag ggcctgcgga ggcggtggca gactagagtt tagatgcccc      240

gagcccaggc agctatttca gcctcctgtt tggtggggtg gcacctgttt cccgggcaat      300

ttaacaatgt ctgaaaaggg actgtgagta atggctgtca cttgtcgggg gcccaagtgg      360

ggtgctctgg tctgaccgat gtgtctccca gaactattct gggggcccga caggtgggcc      420

tgggaggaaa atgtttacat tttttaaaggc acactggtat ttatatttca              470
```

```
<210> SEQ ID NO 511
<211> LENGTH: 193
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 511

gaaaatgaat tccatgttct tgaaggaaag actgtaacta tgtacattca tgatgttcct       60

ttggtgtgtg gtttctgtga gtaacaggta gatgtcattt ctggaaatgg tatgtttatg      120

tctatacatt gttttataaa actccatgga gaaagaaggg gtttacttgc tttgtatcac      180

atagcaataa cat                                                         193
```

```
<210> SEQ ID NO 512
<211> LENGTH: 452
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 512

ctggcccacc caggaacagt gagggcgacg agaactacat ggagttcctc gaggtgctga       60

ccgagggcct tgagcgggtg ctgttggtgc gcggtggtgg ccgtgaagtc atcaccatct      120

actcctgagc ccagtgtcat cttgtggcct ggagtcgagg tcttggccag gacataacaa      180

gctgtggtct ggggtaacag cctcttccca gcacccacct gccagccctg cttgcctggc      240

cctgtcctgg acccagcttt gctaggtctc cttggaaacc aggcctgggc ctcaaaatgg      300

agatggatcc caggtcttgt gggaccctgg gatgtttggg gactttacta tctagcaccc      360

cagtaggcct gtcctggcca gagaagactg gtaggggccg agtggggttt gaaggcagcc      420

ggcccggccc agcccaggag cgctatttat tg                                    452
```

```
<210> SEQ ID NO 513
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 513

ttggaggcct ttgcagcggc ctacaaaggc acgcggccgt ttgccagtgc caacagcgtg       60

ctggacccca tcctcttcta cttcacccag aagaagttcc gccggcgacc acatgagctc      120

ctacagaaac tcacagccaa atggcagagg caggtcgctc gagtcctcca ggtcctgggc      180

agccttcata tttgccattg tgtccgggggc accaggagcc ccaccaaccc caaaccatgc      240

ggagaattag agttcagctc agctgggcat ggagttaaga tccctcacag gacccagaag      300

ctcaccaaaa actatttctt cagccccttc tctggcccag accctgtggg catggagatg      360

gacagacctg ggcctggctc ttgagaggtc ccagtcagcc atggagagct g              411
```

```
<210> SEQ ID NO 514
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
```

<221> NAME/KEY: misc_feature
<222> LOCATION: (110)..(111)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 514

tcgtttctct gaacacacaa cacccatcgt cctctttat gttacttgaa atatcaaaag   60

aattattaca gctgaaaaca aatctatgta aatcggatct tgaaagagan naagctttct   120

ccagtttttga aaggcgccat ttttaacttt gatcttgtaa tgacaaataa gaatgttgaa   180

tcggctggct tttttctatc ctaggtaatg tggactgtgg agctctgtgc tggtcacttt   240

caaccctgaa cctgatgcta cttattttgc agttctaagt gcaaagtcgg cctggtggat   300

gcttcccatt ataatattaa atttgcttct tcgtgaggtc acacctcaca tccccagtgt   360

cactttaata actagtgttt tttacatggt gggccatgac ccattagtgg actctgcatt   420

taa   423

<210> SEQ ID NO 515
<211> LENGTH: 230
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 515

ccctggcaag gcccgggaca ggaaggccta cacggtcctc ctatacggaa acggtccagg   60

ctatgtgctc aaggacggcg cccggccgga tgttaccgag agcgagagcg ggagccccga   120

gtatcggcag cagtcagcag tgcccctgga cgaagagacc cacgcaggcg aggacgtggc   180

ggtgttcgcg cgcggcccgc aggcgcacct ggttcacggc gtgcaggagc   230

<210> SEQ ID NO 516
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 516

atgaccttcg aatgcatagg cctttaatgg tgcagacaga ggaccagtat gttttcctca   60

atcagtgtgt tttggatatt gtcagatccc agaaagactc aaaagtagat cttatctacc   120

agaacacaac tgcaatgaca atctatgaaa accttgcgcc cgtgaccaca tttggaaaga   180

ccaatggtta catcgcctaa ttccaaagga ataacctttc tggagtgaac cagaccgtcg   240

cacccacagc gaaggcacat gcccgatgtc gacatgtttt atatgctaat atcttaattc   300

tttgttctgt tttgtgagaa ctaatttga gggcatgaag ctgcatatca tagatgacaa   360

attggggctg tcgggggctg tggatgggtg gggagcaaat catctgcatt cctgatgacc   420

aatggg   426

<210> SEQ ID NO 517
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 517

gagcaagttg taaattgtct cttatcggac ttaaaagggt gcctggctct tacttagttg   60

attatctcct ggatctggaa agaaaggaag gaaaacaaag gcggaagggg aatctctata   120

gaatgtggat ttttcccaca agagactttg caggcaatt tcaaggtatg cacggaaat   180

atattttggg gttaaatatt tttttccttg tctcataatg ttatgccaga gtcagattga   240

aaagtaaatc acaacatata gggtcaaata aaacccatct gatgagaatg tgtggtttgt   300

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```
agggcatgac ttcctagacc tcttaggtag gaatctgggt aagacagaat atcagactta          360

gtcctcaatt cctaatgcaa agttctgaga tccaaaatgc tccaaaatct aaaacatttt          420

ttagcaccga cataatgcca caagtgga                                             448
```

```
<210> SEQ ID NO 518
<211> LENGTH: 148
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 518

aattaacacc aggaacagca ccttgaatat tcctttttca agttcctctt cctcaggaga           60

tattcaaggt cgaaacacaa gccccaatgt ttctgtacag aaatccaatc ccatgaggat          120

tactgagagt catgccacca agggccac                                             148
```

```
<210> SEQ ID NO 519
<211> LENGTH: 173
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 519

gaaaatcaca actctaacca taatcatctg cactatatgc ctcgcatcag gtaatgtgtc           60

taaaataata agtaacattt agcatttctg accttatccc aaagtatttt aatagtatct          120

gttaatgttt taattaatgg nttttgtatt gcatctcctg gataacaaag tag                 173
```

```
<210> SEQ ID NO 520
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 520

catgagtgtg agctgatttg cacccnanca ccctctgtaa gtgcctgctg tggntttggt           60

tttgattatt ccgttaatgc tgagtctgtt tcacaaacga gattagcaga attaattatt          120

gaagatgcag tatgctttat ggttttaata acactgttaa aaactaaaca aggaagttaa          180

atatgttgat gattatcggt gactgctcac cacacagcat ccctcaggcc gagtcagttg          240

gcccagtgac tcccacatca caaactgccc tttcttggtc agaagaagca gagtggagcc          300

ttctcatccc cacgcgcgca gctgtggggc cccgtggtca cctggccaca tgggagtttg          360

catactgagt ggttcatctt ttccaatgtg ttgtgtcctt taatttacat ttatatttca          420

ttgccctttc taatgatcag a                                                     441
```

```
<210> SEQ ID NO 521
<211> LENGTH: 488
<212> TYPE: DNA
```

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (456)..(456)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 521

tttgagttct gctctggcca atccccaagc tccacgctgt cagccacccc gctctcctac   60

ctcccagagg agcaggctac actcctgttc cttttagaga gagaaatatt gcggccgggc   120

gcggtggctc acgtctgtaa tcccagcatt ttggcaggcc aagggttttg ccatgttcgt   180

ggggctggtc tcaaactaat tacctcagat gatccgccca cctcggcctc ccaaagtgct   240

gggattacag ccgtcctggg ccgccggaca cccccgctgg ggccgatgcc caacagtgac   300

atcgacttga gcaacctgga gcggctggag aagtaccgga gcttcgaccg ctaccggcgc   360

cgggcagagc aggaggcgca ggccccgcac tggtggcgga cctaccgaga gtatttcggg   420

gagaagacag agttccagct tctaaaatat ttgctnctaa aatcttgacc acctgacttt   480

ccggattg   488

<210> SEQ ID NO 522
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (117)..(119)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (228)..(228)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 522

aaaatggatc ctgtctttct tagccaagga ctggtctctt ttctccaatg tgtccctaac   60

agagtggtga ggctggctct tcccaccagt acaggaagat cattccttaa aagaaannnc   120

catatggctt ataagtgttc tttcctgtat gaagcccaag ctgtccactt ggagagacat   180

ctggccagcc ccccgttgtt ccagccatcc ccagttcagg catcaganat gtggtgaaga   240

agccatccta gatgcccagc cccagctacc atctgatgca accacactgc tcaccccgag   300

caagaactgc ctgcaggagc ctagtattat cctctctca   339

<210> SEQ ID NO 523
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 523

gcggcagcaa ccggaaccgg aactcgtcgc ggccaccacc actgagcgct gcggggaggg   60

ggagcaagga ccggacgaga cgctacgcct gaaaacaggc ggcgggcgag ggacgaggct   120

taccacggca ccacgcgagt ggaaagggtc gtctccgcta gcggcggccc acaccagctc   180

accgaggggc ggcagcgcgc ggcccggctg ccggaccgta ccatcccggg cggtggagcc   240

gccgcgcgagg ggcgcgcgcg agccgaaggc gcacccggga ggcccaggta gcccgggggc   300

cggtgctggg gcgccgggca ggcccggctc cgcctcgac ccacccggag ccagcccct   360

ctgcggacac gacatcccca tggggacggt ggcgcg   396

<210> SEQ ID NO 524
<211> LENGTH: 194

-continued

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 524

ccccacaggt gttcctctgt gagctggtcg ggcggccggg gccggggccg ggcttcgctg    60

ctccgtgcct tccacctccc tggcggtgcg gggcctcagg gtgggcctgg gaagctggaa   120

acacctttgg aaacagccgc ctgaggcagc tgtggacaga agaccctgcc cagcagccaa   180

gggagctggc ctct                                                    194


<210> SEQ ID NO 525
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (424)..(430)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (443)..(443)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (445)..(445)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 525

caagggcacg aggcagtacc tttgctccat gcctttgctt ggactagtcc taccaccagc    60

aattcctgca tttctgtgtt tggcaagttt ctgctcagcc tccaaagcct taaccaagtg   120

tcaccttttc tctgcagcat tttctgccac cctccccatt tcttccaata gaaccaggga   180

tcttttactt gggatccaga agcactgtgg acatattgcc atcacaacac ctttcatgtc   240

acaatggcaa ggtttgcact gtcttggagg agaggaagga agccatattc atccctgaac   300

cctcatctcc cagcactggt tgtaaaactg aaacaaaaat ggaaaacctt gatgaaattc   360

attgttggtg tggctatggg gaaacagatt ttccatttct gatagtaaat gaaataggca   420

ccannnnnnn aaaaaaaaaa aananattat taacactgaa aatgcacaca tctttcaacc   480

cagcaatttt atttcttgct ttctagagga atgtttgccc atgtgc                526


<210> SEQ ID NO 526
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 526

cattattaat tataccaatc ctttcatata tgtagaaaaa atgtttgagt tggtcatctg    60

tcttttattg aagatgcatt tcaaatatca aatatatttg aaagataaaa tagcatctgt   120

gaaattgaat attattttat gtgcgcttgg ctatgcccta aaatgtcagt ttattgtccc   180

taaagacgta tttattg                                                 197


<210> SEQ ID NO 527
<211> LENGTH: 275
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 527

ggatgaacgg gtgggctgaa gaacagctga atccaatagc ttggcagaac atgaagacag    60

gtttgttttc cagattctta aaactccaaa cttgatatta ttacagacac aaagtaaatg   120
```

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```
gcacataaca agaggaagga gatcacagtt tgcaaaactt ttatgtggac cttggtactg        180

ggatcttgag atcctttgcc atggaggtgc atcttcttga gatgtttaca cagagaacag        240

actaacagca gaaaagatat cagggttaca gtaaa                                   275


<210> SEQ ID NO 528
<211> LENGTH: 496
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(43)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (46)..(46)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (48)..(48)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 528

aataaatcct gcgagttcac gcccgcgtag ttcgccccct ganttntnga ngcgactcct         60

ttcgcatggg atctacaaaa ccgaactgcc ttaaagacct ctttcacacg gacgtgaagt        120

cacagaactg acaaaatccc atcctgtcaa agtgcacggg tctttgaaat ctaacacaaa        180

aagccataga aagattctct aaacaccctg tactaagagg aacacggaca gggcactgcg        240

ttctgaagta gaggccaggg cactggccct tagacacgtc tcgctgtcac cgggctaaca        300

acattggcaa gggcggcggc agcagcactg atatttgcag cccccaaggg ctctggcgaa        360

accccctcta ttactctgta tcctgcctgc ttccaagatg aacctgttgc tgggaaagaa        420

caggctaaat tagaaaaggg agtattttgt caaagttgaa ggtgagtgat agcctgcccg        480

cctcaaatag gatggg                                                        496


<210> SEQ ID NO 529
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 529

agcgcagtgg cgaggcgagt gtggaaggac tcctgaacca gctcgtcctg gagcacctgc         60

agctggcgcc tctgcagtgg gatgtgctgg tggacggaca gccatgtgac cgcgaggctg        120

tggcggcctg ccaggtgggc gacccggtgc gcctggaggt gcggctgacc aaccggagcc        180

cgcgcagcgt agggcccttc gccctcactg tggtccccct ccaggaccac cagaacggcg        240

tgcacaacta cgacctgcac gacaccgtct ccttcgtggg ctccagcacc ttctacctcg        300

acgcggtgca gccgtccggc cagtcggcct gcctcggggc cctcctcttc ctctacacgg        360

gagacttctt cctccacatc cggttccacg aggacagcac cagcaaggag ctgccaccct        420

cttggttctg cctgcccagt gtgcacgtgt gtgcccctgga ggcgcaggcc tgagcccgcc        480

tacttccgtc cctctttctg cagggccaga ggtgaccctg cctg                         524


<210> SEQ ID NO 530
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 530

aggtcaatct cgtattctct atgtgatatt gctgacaaag tcaaagtaag gaaagacata      60

tcaagggaag gcaatggaag cacctttct ttatagtaca ttcacctacc ttaacagacc      120

aagataacat aggagagaaa ctggggctta agtccttgat agagcttctg ggggcacagt     180

agttataggg ccaggtcaga aaatgtcctc acacactaag aaggcattt aaaatcagaa       240

aagacagtca cactcacttt ggtcaccaag tcatttagcc atcctgtctg gaaagcatgt     300

tttcctctgg ggtcttcctc tggggtatct tgggaaaggg tagagttttg aggagctaga    360

gaagagaaag aggtcatgag ggagattagt cctttctgaa tagcctagga aacccctcac    420

caaatagatg cctacacttt cttaaatcga gaagtaagaa ggaaatcaaa aacagcactc    480

ctacttcaaa gcatcag                                                    497


<210> SEQ ID NO 531
<211> LENGTH: 253
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 531

gtgaaaagca accaaaggca acagagtcta gctcatggcc accagaccaa aagcatccag      60

cttctgtgca cctcctgcaa agctggcaga ggccctggaa ttccagatca cctgagggga     120

aagggttgtc tctctccttt ctgttggggg aggggatgg gggactttg ttggtggctc       180

ccacccatat atccctcctt taccatagta ctcccaccca cttccatcac ccatccaata    240

aaatgcagcc agg                                                        253


<210> SEQ ID NO 532
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 532

cacctcggtc accagtgtga accaagccag cacatcccgc ctggagggcc tacagtcaga      60

aaaccatcgc ctgcgaatga agatcacaga gctggataaa gacttggaag aggtcaccat     120

gcagctgcag gacacaccag aaaagaccac ctacattaaa cagaaccact accaagagct    180

caatgacatc ctcaacctgg aaacttcac tgagagcaca gatggaggaa aggccatttt     240

aaaaaatcac ctcgatcaaa atccccagct acagtggaac acaacagagc cctctcgaac    300

atgcaaagat cctatagaag atataaactc tccagaacac atccagcgtc ggctgtccct    360

ccagctcccc atcctccacc acgcctacct cccatccatc ggaggcgtgg acgccagctg    420

tgtcagcccc tgcgtcagcc ccaccgccag ccccgccac agacatgtgc caccctcctt     480

ccgagtcatg gtctcgggcc tgtaagggtg gggggcctgg gcccggggcc tcccccgtga    540

cagaaccaca ctgggcagag gggtctg                                         567


<210> SEQ ID NO 533
<211> LENGTH: 402
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 533

cagtattctg taccatagcg ctgctcttat gccatttgtt tatttttata tagcttgaaa      60

catagaggga gagagggaga gagcctatac cccttactta gcatgcacaa agtgtattca     120
```

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```
cgtgcagcag caacacaatg ttattcgttt tgtctacgtt tagtttccgt ttccaggtgt        180

ttatagtggt gttttaaaga gaatgtagac ctgtgagaaa acgttttgtt tgaaaaagca        240

gacagaagtc actcaattgt ttttgttgtg gtctgagcca aagagaatgc cattctcttg        300

ggtgggtaag actaaatctg taagctcttt gaaacaactt tctcttgtaa acgtttcagt        360

aataaaacat ctttccagtc cttggtcagt ttggttgtgt aa                           402
```

```
<210> SEQ ID NO 534
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (178)..(178)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 534
```

```
tgcattgtac ctgtagccat tccattgtga ataacacaaa aagtggagga aatattttc          60

tcgcatttgg aaattattct gtgattcagc aaagaagttg ttcatgtcat taacaagttc        120

agaaatacat gctgccaaag ccaaaaagag tcttcagttt aataaaaata attaacanga        180

aggtgagaaa tggtttacca gctgttcact tactggattt aaggttactt gttggggaaa        240

gagcagagta agatgcaact ctgtcaaatc atggctgaa                               279
```

```
<210> SEQ ID NO 535
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 535
```

```
tagcaaagga catggaagcc tggaaagatg taaccagtgg aaatgctaaa atttaccagc         60

ttccagggg tcacttttat cttctggatc ctgcgaacga gaaattaatc aagaactaca        120

taatcaagtg tctagaagta tcatcgatat ccaattttta gatattttcc ctttcacttt        180

taaaataatc aaagtaatat catactcttc tcagttattc agatatagct cagttttatt        240

cagattggaa attacacatt ttctactgtc agggagattt gttacataaa tatatttacg        300

tatctgggga caaaggtcaa gccagtaaag aatacttctg gcagcacttt ggga              354
```

```
<210> SEQ ID NO 536
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (304)..(306)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (308)..(309)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (311)..(313)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (315)..(317)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

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```
<222> LOCATION: (354)..(354)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (361)..(361)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 536

ttccctgatg actcacttac aagttagtga actccttgtt taagtattac aaactgcaca        60

ccttctccct tctcaatcta gcttcacatc aggccttcct gccaaagcgg caaacttgcc       120

acatggggca aggtactccc caagcagaca aggcccatct gtgtcatgag tgatacccaa       180

tgctaatgcc atgctctgaa atgtagtgcc caccttggct tcccaaagtg ctgggattgc       240

agacgtgagt cactgcgccc agccattcca tgtctcttaa gtctcagaat ctcccctagc       300

tncnnncnng nnncnnnagt ggttgtcccc tcaaagctgt cccacaccct cctncgagga       360

ncctttgtgt atctcctcca gctaccgcag agcccacaaa cccaggcatc tatcaaagtc       420

cctcattcat gagggtggtg aggacacaga ctgcgaccag aacagaaata tgaaaatgtg       480

aatgacagcg tcccccg                                                       497


<210> SEQ ID NO 537
<211> LENGTH: 340
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (115)..(115)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (118)..(118)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 537

tggagttagc aaaccttttc atgcctgtga cctcactgga gttctttgat gttgggactt        60

cataagtntg ccaaatcctg ncacttactg ctttatgacc ttgaccattt accgnttntn       120

tntggacctc agtgttctca ggatgcaaaa ggagggtcag gggtaaaata gcgactttcg       180

aactgtcagg ggtaaaatag cgactttcaa acttttcaaa cttctgggac aagggtgaag       240

ggcaggactc tgcctctctc cttcccttca ccttattcca cttaaattgt gtgattctac       300

aagcttatgt ttaaaggaat atgttcctcc attacaaaga                             340


<210> SEQ ID NO 538
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (133)..(133)
```

<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (148)..(148)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 538

```
tgggaccacg ggcatttttg gcatgtacaa gggtataggt gcctcctact tccgcctcgg      60

cccccacacc atcctctccc tcttcttctg ggaccagctg cgctccctct actacacaga     120

cactaaataa canccgcttt cccagtcntc caccaaatga gcactccttg gccacttgtg     180

cctccaccac tatgtcctgg tgactactga ttaggtgacc tttcatccat ccatggggga     240

cagccaaccc cactccccat ctgttctcag ggttgaatca ctacaagaga tgagtttccc     300

ttctttcctt gggtgttgct ttaaaccttc cctacccatt ccctgggtaa ctcacacccc     360

tctctcaggg ctgaacgagt catcccaaag tgtatttcct cccactcacc actgccaccc     420

ttgagtccct cctgctccca tgcacagttt taaactcctc cctccaaaac caaagggaat     480

tgagagaccc aattcccagg cgtctgggac ccaggtgtcc tgttaga                   527
```

<210> SEQ ID NO 539
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 539

```
gacatgtttt ctagccttag ttccccatct acaaaatggg cctcatggaa tggaatgtct      60

ccacttcact ccagcatcaa caagtgggga attctgatgg attcaattcg acttctttcc     120

atgggcgtgt ctaagcagc ctctttgttc cagaagctgc cctcagccag agttggataa     180

gccaatcctc actccccagc ctcctctgga tagggatgaa gaccccactg gggttggaag     240

tgcagaggca gacaggtgta tggagtcacc tgtaaattga ttcaagtgag ccaggaaagc     300

agcaaaggaa agagaaacct gagtgacgac gtggtggagg aacagggctg gaaagaggct     360

gctggctgtc tggcttcgca gctctggcct cctaatcagc ctcgctcttg tctctggtgt     420

tctctggctc ttgtccatct gtctgtgttt cttttttgcca gctattgact aatctttgct     480

gaagctgagc tagaattctg gtgtttataa gcaggtaact agctgagcac ta             532
```

<210> SEQ ID NO 540
<211> LENGTH: 811
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 540

```
ctttgggagg ctgaggcagg cagatcacct aaggccagga attcgacacc agcctggcca      60

acgtggcaaa acccgtctct actaaaaata caaaaattag ccgggcgtgg tggtgtgcgc     120

ctggaatccc agctacccag gaggctgagg caggagaaat gctggaaccc gggaggcaga     180

ggctgcagtg agctgagatc atgccactac tgcactccag cctgggtgac acagcaagac     240

tccctctaaa aaagaaaaa aagaaaagaa aagaaaagaa aatgatatat ccatgatgaa     300

ttaaaatgga gtggaaccca ctgatgggaa agccacagaa ggtaccagtt atccactcac     360

tgacttaggt gcctccacta gaattctcag cacgtttttg cagaacctgg gcaacaagag     420

cgaaacccca tctcaaaacc acaacaacaa caacaggaca acagagatgg acgacggatc     480

gggaaagcca accagacagc gtgaggccag gacggaaaga ggcacaggga gctctgctca     540

gtgtcgctac aggggatctc tcaggctcac aacgggccac tcctctaggg aagttctggt     600
```

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```
ctcatcatga tccttgtttg gtctcactcc ccatgtcctt ctctgtccct cctccaactg      660

ccatttattt atttaactga aaaagtacca atcacccaca taggcatgac atactcatcc      720

atgtacccat ttcttaaaat tgatcattgt taacatttgg tgtaatttgc tttatttatt      780

tttaatgaaa taaataaaac tttacagaaa a                                     811


<210> SEQ ID NO 541
<211> LENGTH: 3874
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 541

aaaaaggtac aactaccttg ctgatgctgt acatatggct cacttgtgcc cagagagaga       60

ataaagccat gtcgaaacta tctacgattc cttgagtgtt tttccagcta cctgccactt      120

gcccacccac tcccctcaga tctcagttag aacatgacaa ttgggctcat gaacaggatc      180

ctgagtggtt gcaggtgaac aagcagttgg cacaagggca aagtgatcac atcctgattg      240

agtggctatg gacagccata cagactgtgt ggaacaacgc tggtgaaata cccaaaccat      300

ttagaagcag taatgcctca cttgcctggg actgggatgg tgtggctgag actgccttac      360

tggcagccag gtgcgctatt cagcagccac aagccctaca agtaattaac caggggcacc      420

tgtttgagct ggaggtgcat gtggccacag acggttttgg ttgaggcttg tggcaatgca      480

cagagcgcct aagaatgcca gtaggctttt ggtcccaact atggaaagga gctgaactcc      540

ggtattcatt gatagagaaa cagctagcag ctgtatatgc tggccttcgg gctcatgaga      600

gcatgacagg acaggctgca gtcatcatat ggacaactta cccaataaca ggatggatgc      660

gtctatgtgt aatgaccacc tggagtggga tagcacagat gtccactttg gcaaaatggg      720

gcgactcctt gcagcagtgg agtaagctga gtacaagtcc catagcagca gagttgcaag      780

aggtcttggg acgtgtagtc ctaatgcaag ataaggccat gcggcctgag gcacccctag      840

atcctgagtc ttcaccattt aaggaagggc atcccaggat tcctgagggg gcatggtaca      900

cagtagatga ggtgctactg ctgcctggac cactgttgca gtccaaccta gtactgacac      960

catatggttt gaaactgggt gcggacaaag tagccaatgg gctgaactca gagcagtgtg     1020

gatggtaatc accaaggagg tgacacctgt ggtaatctgt actgatagct gggcagtcta     1080

ctgaggctta accttgtggt taactacttg gaaaatacag aattggctag tgagccacag     1140

acccatttga ggccaagcca tatggcaaga cctttgggga ataggtcatc aaaaagaggt     1200

aactatttat catgtgtcag gccatatgcc tttggccacc cctagtaatg atgaggcaga     1260

tgccttggct aaggtcagat ggtcagagtc agcaccaaca caagatgtga ccttgtggct     1320

acaccggaaa ctgggacatg cagggggtaa actgatgtaa caattcaata agtgttgggg     1380

tctgtccctt cccaagcaag acatttgtga ggcttgtcag aaatgcctgg catgtgttca     1440

gacatatcct aaaaagaggc agctgcccgg tgttatacaa caagtaacaa tagggtgagt     1500

gcccttgacc aggtgggaag tagactacat cgggccgccg ccaaagtcgc gagggtatac     1560

gcatgcacta acggctgtag acatggccac aggcctgttg ttcacctacc cttgcagggt     1620

ggccaaccaa cagaacacca tccaggccct gcaacactta tgttccctgt atggttgtcc     1680

tctggccatt gagagtgata ggggaacaca tttcactgga caacaggtac aatgatgggc     1740

acagcaaatg gacataaagt gggggattcca tgtgccatac agcccacaag ctgaggtatt     1800

attgaatgat ataatgggat cttgaagaat ggattacgct tgcatgtcaa acccctgtct     1860
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ttgcggagct ggagttccag gctggacctg gtgctccaaa ccttaaatga atggccacag      1920

aaaggtggcc cggcccccagt ggaggctttg tttcactagg ccaccacccc cattcaattg      1980

gagatacata ccaaggatga cctcctccga tcaggtatgg ggacaaatgg taacctgttg      2040

ttgcctgccc caacaaccct gaaggcaggg gaacagaaaa cctggctgtg gccatggacc      2100

ctccaagctc tccactgctg gtggttggcc atcatagctc cctgtgggga gggcctacag      2160

tatgacttgc atgtcacttt ttgagtgttc aatacatggc ttccaaggtt gactgtttgt      2220

agaggaacag ccagggaagg aaccctcctc tgagggacat atgtactatc tgatgggcct      2280

attatgagct acgctgtgac tttggcatgg atacaggatt ctaaggaacc atggagattt      2340

gagaaggtgt ggtaccatca cccagggcaa aagcccttgg tggctgcatt gttatccagg      2400

gatggaaagt tagcctatat tttgcctgag ggatgtgatt tacctctgtt agtacctgtg      2460

cctgctctgt catttcaacc gtaggttaac atgctccaat tgcattgtgg actgacccca      2520

cacctatgct gaggtgacca atgtttccaa ctgttggacc tgcactgcct ttccagcagc      2580

agctgcagac agcttgcccc gacacataca tcccgtgtct gcagagaact ggacatgcct      2640

ggagacttga gatcccatgg ctgatgcctg aacacaatg tggcaagctt tggacaaagg      2700

acacagcaag acccatggct ggaccgtagc attcgtgatg agtggggctg gctagtaggg      2760

gaacatgtag tagcccaagc ccaggcattg cagtgcacag agcaacattg gggtaacagg      2820

atgggtacct gtcacggcct gtgcaaacat aacatgtgtc accacactga aggtatggta      2880

gaacaagtgg cctcaccaag gtcggacccc aatggacttt ttgcctcttg ggagcttatg      2940

ggtctatgag gacacagtag cctttcctat cagcaaactg gagtggatgt tgtatctggg      3000

ggtggcctta tgtacctgct actgttctcc ccacattgcc cagatgcctg tataactggg      3060

aggcactgtg ctctcagttt ttgcgaatgt gatgagcccc ctggtgtttc tacccttttgg      3120

caatgactat ccctggagca ggtgtcaaaa ctgtagaagc acaatttact gctcttgcgg      3180

agcacaccgc tcaggctctg aattacacct gagtgtccct cctcctgtta atgaatgagg      3240

ttgatcagat caaaaagtgg tgttgcaaaa ccaagtggcc ttagacataa ctgctgccca      3300

aggagccacc tgtgcccttt taggaacaca atgttgtacc ttatccctga caatcagcag      3360

aacataacag cagccctgca aaggggtctt ccaggagatt aaggtgactg agagcctcac      3420

tgtcaacccc ctgcagagat ggtgagcatc cctaggttct ggcgtacatt gggccctaat      3480

agtcataagt atcatagctg agatcctagt agtgagctgt tgctctctgt attgttgttg      3540

tgggttatgg actcagggct ccgccatata ggcatgtgtc cctgcctgga ggacgccctc      3600

agcctagggg gtgtagtgta agggaaatgg ctgtgcttta gtcaggagta ggctgaggca      3660

gccttctggt gcagcatgac tcagtgggtt tggagtgcaa gcacacaacc ttgctcgtta      3720

tgtaaccaca ccacatgagg cccattaggt aacaactcac atgagctcgt gtttggctca      3780

gagccactat tgtctgtaaa aggtatacct tgctgatgct gcacatatgg ctcgcttgtg      3840

cccagagaga gagtaaagcc atgttgaaac tgtc                                  3874
```

```
<210> SEQ ID NO 542
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 542

Met Pro Val Gly Phe Trp Ser Gln Leu Trp Lys Gly Ala Glu Leu Arg
1               5                   10                  15
```

```
Tyr Ser Leu Ile Glu Lys Gln Leu Ala Ala Val Tyr Ala Gly Leu Arg
            20                  25                  30

Ala His Glu Ser Met Thr Gly Gln Ala Ala Val Ile Ile Trp Thr Thr
        35                  40                  45

Tyr Pro Ile Thr Gly Trp Met Arg Leu Cys Val Met Thr Thr Trp Ser
    50                  55                  60

Gly Ile Ala Gln Met Ser Thr Leu Ala Lys Trp Gly Asp Ser Leu Gln
65                  70                  75                  80

Gln Trp Ser Lys Leu Ser Thr Ser Pro Ile Ala Ala Glu Leu Gln Glu
                85                  90                  95

Val Leu Gly Arg Val Val Leu Met Gln Asp Lys Ala Met Arg Pro Glu
            100                 105                 110

Ala Pro Leu Asp Pro Glu Ser Ser Pro Phe Lys Glu Gly His Pro Arg
            115                 120                 125

Ile Pro Glu Gly Ala Trp Tyr Thr Val Asp Glu Val Leu Leu Leu Pro
    130                 135                 140

Gly Pro Leu Leu Gln Ser Asn Leu Val Leu Thr Pro Tyr Gly Leu Lys
145                 150                 155                 160

Leu Gly Ala Asp Lys Val Ala Asn Gly Leu Asn Ser Glu Gln Cys Gly
                165                 170                 175

Trp


<210> SEQ ID NO 543
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 543

catgaacagg atcctgagtg g                                           21


<210> SEQ ID NO 544
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 544

tgaggcatta ctgcttctaa atgg                                        24


<210> SEQ ID NO 545
<211> LENGTH: 2863
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 545

cacgccaaac acgcagcccc ctcccgctgg agtgacaact ggccagcata ctctaggctg    60

ttgtcccttt aaaacttgaa tccaaggggg taatgattta tcaaacttgt attatcaaga   120

aaatgtcaaa ccaagggcac cttgctttgc actgacgcaa acccggcctt tcccaaggag   180

atatagaaag cgcctctcct gcctgagcca aacccagtct tgtcaatagc gggtttcacc   240

ctccaccagt tcagtctgtt gcctgtgtca gacatggatt gcagtgctcc caaggaaatg   300

aataaactgc cagccaacag cccggaggcg gcggcggcgc agggccaccc ggatggcccca   360

tgcgctccca ggacgagccc ggagcaggag cttcccgcgg ctgccgcccc gccgccgcca   420
```

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cgtgtgccca ggtccgcttc caccggcgcc caaactttcc agtcagcgga cgcgcgagcc      480

tgcgaggctg agcggccagg agtggggtct tgcaaactca gtagcccgcg ggcgcaggcg      540

gcctctgcag ctctgcggga cttgagagag gcgcaaggcg cgcaggcctc gcccctccc      600

gggagctccg ggcccggcaa cgcgctgcac tgtaagatcc cttttctgcg aggcccggag      660

ggggatgcga acgtgagtgt gggcaagggc accctggagc ggaacaatac ccctgttgtg      720

ggctgggtga acatgagcca gagcaccgtg gtgctggcca cggatggaat cacgtccgtg      780

ctcccgggca gcgtggccac cgttgccacc caggaggacg agcaaggggga tgagaataag      840

gccccgaggga actggtccag caaactggac ttcatcctgt ccatggtggg gtacgcagtg      900

gggctgggca atgtctggag gtttccctac ctggccttcc agaacggggg aggtgctttc      960

ctcatccctt acctgatgat gctggctctg gctggattac ccatcttctt cttggaggtg     1020

tcgctgggcc agtttgccag ccagggacca gtgtctgtgt ggaaggccat cccagctcta     1080

caaggctgtg gcatcgcgat gctgatcatc tctgtcctaa tagccatata ctacaatgtg     1140

attatttgct atacactttt ctacctgttt gcctcctttg tgtctgtact accctggggc     1200

tcctgcaaca acccttggaa tacgccagaa tgcaaagata aaaccaaact tttattagat     1260

tcctgtgtta tcagtgacca tcccaaaata cagatcaaga actcgacttt ctgcatgacc     1320

gcttatccca acgtgacaat ggttaatttc accagccagg ccaataagac atttgtcagt     1380

ggaagtgaag agtacttcaa gtactttgtg ctgaagattt ctgcagggat tgaatatcct     1440

ggcgagatca ggtggccact agctctctgc ctcttcctgg cttgggtcat tgtgtatgca     1500

tcattggcta aaggaatcaa gacttcagga aaagtggtgt acttcacggc cacgttcccg     1560

tatgtcgtac tcgtgatcct cctcatccga ggagtcaccc tgcctggagc tggagctggg     1620

atctggtact tcatcacacc caagtgggag aaactcacgg atgccacggt gtggaaagat     1680

gctgccactc agattttctt ctctttatct gctgcatggg gaggcctgat cactctctct     1740

tcttacaaca aattccacaa caactgctac agggacactc taattgtcac ctgcaccaac     1800

agtgccacaa gcatctttgc cggcttcgtc atcttctccg ttatcggctt catggccaat     1860

gaacgcaaag tcaacattga gaatgtggca gaccaagggc caggcattgc atttgtggtt     1920

tacccggaag ccttaaccag gctgcctctc tctccgttct gggccatcat cttttttcctg     1980

atgctcctca ctcttggact tgacactatg tttgccacca tcgagaccat agtgacctcc     2040

atctcagacg agtttcccaa gtacctacgc acacacaagc cagtgtttac tctgggctgc     2100

tgcatttgtt tcttcatcat gggttttcca atgatcactc agggtggaat ttacatgttt     2160

cagcttgtgg acacctatgc tgcctcctat gcccttgtca tcattgccat ttttgagctc     2220

gtggggatct cttatgtgta tggcttgcaa agattctgtg aagatataga gatgatgatt     2280

ggattccagc ctaacatctt ctggaaagtc tgctgggcat ttgtaacccc aaccatttta     2340

acctttatcc tttgcttcag cttttaccag tgggagccca tgacctatgg ctcttaccgc     2400

tatcctaact ggtccatggt gctcggatgg ctaatgctcg cctgttccgt catctggatc     2460

ccaattatgt ttgtgataaa aatgcatctg gccctggaa gatttattga gaggctgaag     2520

ttggtgtgct cgccacagcc ggactggggc ccattcttag ctcaacaccg cggggagcgt     2580

tacaagaaca tgatcgaccc cttgggaacc tcttccttgg gactcaaact gccagtgaag     2640

gatttggaac tggcactca gtgctagtcc agtggtgtgg gatggtccag acttgatcct     2700

gttttttcctc tctgcctcct cctaatgttt tccatagctc tcctcccatt tttcttcatc     2760
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tttcttccta catcttggtt cacatccacg catgagagtg attatgtaga aaagtaggca      2820

tagtgtcgca tgctgcagta aagagctaca tagaccacct gaa                        2863


<210> SEQ ID NO 546
<211> LENGTH: 797
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 546

Met Asp Cys Ser Ala Pro Lys Glu Met Asn Lys Leu Pro Ala Asn Ser
1               5                   10                  15

Pro Glu Ala Ala Ala Ala Gln Gly His Pro Asp Gly Pro Cys Ala Pro
            20                  25                  30

Arg Thr Ser Pro Glu Gln Glu Leu Pro Ala Ala Ala Ala Pro Pro Pro
        35                  40                  45

Pro Arg Val Pro Arg Ser Ala Ser Thr Gly Ala Gln Thr Phe Gln Ser
    50                  55                  60

Ala Asp Ala Arg Ala Cys Glu Ala Glu Arg Pro Gly Val Gly Ser Cys
65                  70                  75                  80

Lys Leu Ser Ser Pro Arg Ala Gln Ala Ala Ser Ala Ala Leu Arg Asp
                85                  90                  95

Leu Arg Glu Ala Gln Gly Ala Gln Ala Ser Pro Pro Pro Gly Ser Ser
            100                 105                 110

Gly Pro Gly Asn Ala Leu His Cys Lys Ile Pro Phe Leu Arg Gly Pro
        115                 120                 125

Glu Gly Asp Ala Asn Val Ser Val Gly Lys Gly Thr Leu Glu Arg Asn
    130                 135                 140

Asn Thr Pro Val Val Gly Trp Val Asn Met Ser Gln Ser Thr Val Val
145                 150                 155                 160

Leu Ala Thr Asp Gly Ile Thr Ser Val Leu Pro Gly Ser Val Ala Thr
                165                 170                 175

Val Ala Thr Gln Glu Asp Glu Gln Gly Asp Glu Asn Lys Ala Arg Gly
            180                 185                 190

Asn Trp Ser Ser Lys Leu Asp Phe Ile Leu Ser Met Val Gly Tyr Ala
        195                 200                 205

Val Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu Ala Phe Gln Asn
    210                 215                 220

Gly Gly Gly Ala Phe Leu Ile Pro Tyr Leu Met Met Leu Ala Leu Ala
225                 230                 235                 240

Gly Leu Pro Ile Phe Phe Leu Glu Val Ser Leu Gly Gln Phe Ala Ser
                245                 250                 255

Gln Gly Pro Val Ser Val Trp Lys Ala Ile Pro Ala Leu Gln Gly Cys
            260                 265                 270

Gly Ile Ala Met Leu Ile Ile Ser Val Leu Ile Ala Ile Tyr Tyr Asn
        275                 280                 285

Val Ile Ile Cys Tyr Thr Leu Phe Tyr Leu Phe Ala Ser Phe Val Ser
    290                 295                 300

Val Leu Pro Trp Gly Ser Cys Asn Asn Pro Trp Asn Thr Pro Glu Cys
305                 310                 315                 320

Lys Asp Lys Thr Lys Leu Leu Leu Asp Ser Cys Val Ile Ser Asp His
                325                 330                 335

Pro Lys Ile Gln Ile Lys Asn Ser Thr Phe Cys Met Thr Ala Tyr Pro
            340                 345                 350

Asn Val Thr Met Val Asn Phe Thr Ser Gln Ala Asn Lys Thr Phe Val
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          355                  360                  365

Ser Gly Ser Glu Glu Tyr Phe Lys Tyr Phe Val Leu Lys Ile Ser Ala
    370                  375                  380

Gly Ile Glu Tyr Pro Gly Glu Ile Arg Trp Pro Leu Ala Leu Cys Leu
385                  390                  395                  400

Phe Leu Ala Trp Val Ile Val Tyr Ala Ser Leu Ala Lys Gly Ile Lys
                405                  410                  415

Thr Ser Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Tyr Val Val
                420                  425                  430

Leu Val Ile Leu Leu Ile Arg Gly Val Thr Leu Pro Gly Ala Gly Ala
                435                  440                  445

Gly Ile Trp Tyr Phe Ile Thr Pro Lys Trp Glu Lys Leu Thr Asp Ala
    450                  455                  460

Thr Val Trp Lys Asp Ala Ala Thr Gln Ile Phe Phe Ser Leu Ser Ala
465                  470                  475                  480

Ala Trp Gly Gly Leu Ile Thr Leu Ser Ser Tyr Asn Lys Phe His Asn
                485                  490                  495

Asn Cys Tyr Arg Asp Thr Leu Ile Val Thr Cys Thr Asn Ser Ala Thr
                500                  505                  510

Ser Ile Phe Ala Gly Phe Val Ile Phe Ser Val Ile Gly Phe Met Ala
                515                  520                  525

Asn Glu Arg Lys Val Asn Ile Glu Asn Val Ala Asp Gln Gly Pro Gly
    530                  535                  540

Ile Ala Phe Val Val Tyr Pro Glu Ala Leu Thr Arg Leu Pro Leu Ser
545                  550                  555                  560

Pro Phe Trp Ala Ile Ile Phe Phe Leu Met Leu Leu Thr Leu Gly Leu
                565                  570                  575

Asp Thr Met Phe Ala Thr Ile Glu Thr Ile Val Thr Ser Ile Ser Asp
                580                  585                  590

Glu Phe Pro Lys Tyr Leu Arg Thr His Lys Pro Val Phe Thr Leu Gly
    595                  600                  605

Cys Cys Ile Cys Phe Phe Ile Met Gly Phe Pro Met Ile Thr Gln Gly
    610                  615                  620

Gly Ile Tyr Met Phe Gln Leu Val Asp Thr Tyr Ala Ala Ser Tyr Ala
625                  630                  635                  640

Leu Val Ile Ile Ala Ile Phe Glu Leu Val Gly Ile Ser Tyr Val Tyr
                645                  650                  655

Gly Leu Gln Arg Phe Cys Glu Asp Ile Glu Met Met Ile Gly Phe Gln
                660                  665                  670

Pro Asn Ile Phe Trp Lys Val Cys Trp Ala Phe Val Thr Pro Thr Ile
    675                  680                  685

Leu Thr Phe Ile Leu Cys Phe Ser Phe Tyr Gln Trp Glu Pro Met Thr
    690                  695                  700

Tyr Gly Ser Tyr Arg Tyr Pro Asn Trp Ser Met Val Leu Gly Trp Leu
705                  710                  715                  720

Met Leu Ala Cys Ser Val Ile Trp Ile Pro Ile Met Phe Val Ile Lys
                725                  730                  735

Met His Leu Ala Pro Gly Arg Phe Ile Glu Arg Leu Lys Leu Val Cys
                740                  745                  750

Ser Pro Gln Pro Asp Trp Gly Pro Phe Leu Ala Gln His Arg Gly Glu
    755                  760                  765

Arg Tyr Lys Asn Met Ile Asp Pro Leu Gly Thr Ser Ser Leu Gly Leu
770                  775                  780
```

```
Lys Leu Pro Val Lys Asp Leu Glu Leu Gly Thr Gln Cys
785                 790                 795
```

```
<210> SEQ ID NO 547
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 547

ggatttgcaa gttgtgtagt gtgc                                                24
```

```
<210> SEQ ID NO 548
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 548

aagcagatgg tcatcttcca g                                                   21
```

```
<210> SEQ ID NO 549
<211> LENGTH: 2426
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 549

ctctttcaac tcaagagctc agtcctgtgt ctctcatgga ggcgtctcta accaggaggc      60

tactctttaa agacaggcat tttacttgca gcaaaataat aggaaggaga ttcgcttgct     120

ttgcacagag gctgagccac aggagaaagc aaagccaatg tgatttattg aatgaaagca     180

ctggacaatt accaacaact tgttcctctg ctgcctcgaa cagcataaac tggaattgtc     240

gtgtgaaaat gacgcaacaa atgcaaaatt tacatctctg tcagtcaaaa aaacatagtg     300

ctccctcatc tcccaacgca gccaaacgcc tgtacaggaa cctctctgag aaactgaaag     360

ggagccactc ttccttcgat gaggcctatt ttaggacaag aactgatcgg ctgagtctca     420

ggaagacctc ggtgaatttc cagggcaatg aagccatgtt tgaggcagtc gaacagcagg     480

acatggatgc tgtgcagatc tcctgtatc agtacacacc agaagaactt gacctcaaca      540

cacctaacag cgagggcttg acacccctgg atattgccat catgaccaac aatgtgccca     600

ttgcaaggat tcttctgagg acaggggccc gagaaagtcc acactttgtc agcctggaaa     660

gccgagcaat gcacctcaac acactggtcc aggaagccca ggagagggtg agtgaactgt     720

ctgcccaggt ggagaatgaa ggattcactc tggacaacac agagaaagag aagcagctga     780

aagcttggga gtggaggtat cggctctaca gacgcatgaa aacaggcttt gagcatgcca     840

gagcccctga gatgccaacc aatgtctgtc tcatggtaac cagcagcaca tcactcactg     900

tcagcttcca gagcctctt agcgtcaatg cagctgtagt aaccaggtat aaagtggaat      960

ggagtatgtc cgaagacttt tctcctttgg ctggagaaat catcatggat aatctgcaga     1020

ctctgagatg cacaatcaca ggacttacaa tgggccaaca gtattttgtt caagtctcgg     1080

cttacaatat gaaaggatgg ggacctgctc agaccacgac accggcatgt gcctctcctt     1140

ctaactggaa agactatgac gacagagagc ccagacacaa gggacagagt gaagttttgg     1200

aaggtctgct gcagcaggtc cgagcccttc atcagcatta cagttgccgg gaaaagcacaa    1260
```

```
aattacaaac cacaggccgc aagcagtcag tctcaagaag cctgaaacac ctgttccatt        1320

cctcgaacaa gtttgtgaag accttaaaac ggggactcta catagccgtt atattttatt        1380

acaaagacaa tatcttagtc accaatgaag atcaagtacc aattgttgaa atagatgact        1440

ctcacaccag ttctattaca caagattttc tgtggttcac gaagctgtct tgtatgtggg        1500

aagatataag gtggctgagg caaagcatac caatatcctc atcctcatcc acagtgctgc        1560

aaactcggca gaagatgctc gcagcaacag cacagctaca gaatttactt gggacacaca        1620

acttgggaag agtttactat gagcccatta agatcgaca tggaaacata ctcatagtca         1680

ccatcaggga ggtggagatg ctttattcat tttttaatgg caaatggatg cagatctcaa        1740

agctgcaaag ccagagaaag tctctatcaa cacctgagga gccaacagct ttagacattc        1800

tactgataac catccaggat attctatcct atcacaaaag gagtcatcag cgtctctttc        1860

ctggattata tctgggttac ctaaagctct gtagctctgt ggatcaaatc aaagttcttg        1920

ttacccaaaa gttgcccaac attctctgcc acgtgaagat ccgtgaaaac aataatattt        1980

ctagagagga atgggaatgg atccaaaagc tttctggctc tgaatctatg gaaagtgtgg        2040

atcatacttc tgactgcccc atgcaattgt tcttctacga gctccagatg gcagtgaaag        2100

ctctccttca gcagatcaat atacctctac accaggcaag gaacttccgc ctctacacac        2160

aggaggtgtt ggaaatgggt cacaatgtgt cctttcttct cctgctccct gcctcagacg        2220

acgtctgtac agccccagga cagaataatc cttacacccc acactcaggg tttcttaacc        2280

tccctcttca gatgtttgaa cttggtatag tagcttgttt cacctagaaa tattaaccca        2340

gcctccttat aataaaatca caagttata tctgttcccc cttgtcccag tggagggtca        2400

ataaatcaca tgatggcttt ggcaac                                             2426
```

<210> SEQ ID NO 550
<211> LENGTH: 763
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 550

```
Met Glu Ala Ser Leu Thr Arg Arg Leu Leu Phe Lys Asp Arg His Phe
1               5                   10                  15

Thr Cys Ser Lys Ile Ile Gly Arg Arg Phe Ala Cys Phe Ala Gln Arg
                20                  25                  30

Leu Ser His Arg Arg Lys Gln Ser Gln Cys Asp Leu Leu Asn Glu Ser
        35                  40                  45

Thr Gly Gln Leu Pro Thr Thr Cys Ser Ser Ala Ala Ser Asn Ser Ile
    50                  55                  60

Asn Trp Asn Cys Arg Val Lys Met Thr Gln Gln Met Gln Asn Leu His
65                  70                  75                  80

Leu Cys Gln Ser Lys Lys His Ser Ala Pro Ser Ser Pro Asn Ala Ala
                85                  90                  95

Lys Arg Leu Tyr Arg Asn Leu Ser Glu Lys Leu Lys Gly Ser His Ser
                100                 105                 110

Ser Phe Asp Glu Ala Tyr Phe Arg Thr Arg Thr Asp Arg Leu Ser Leu
        115                 120                 125

Arg Lys Thr Ser Val Asn Phe Gln Gly Asn Glu Ala Met Phe Glu Ala
    130                 135                 140

Val Glu Gln Gln Asp Met Asp Ala Val Gln Ile Leu Leu Tyr Gln Tyr
145                 150                 155                 160
```

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```
Thr Pro Glu Glu Leu Asp Leu Asn Thr Pro Asn Ser Glu Gly Leu Thr
                165                 170                 175

Pro Leu Asp Ile Ala Ile Met Thr Asn Asn Val Pro Ile Ala Arg Ile
            180                 185                 190

Leu Leu Arg Thr Gly Ala Arg Glu Ser Pro His Phe Val Ser Leu Glu
            195                 200                 205

Ser Arg Ala Met His Leu Asn Thr Leu Val Gln Glu Ala Gln Glu Arg
    210                 215                 220

Val Ser Glu Leu Ser Ala Gln Val Glu Asn Glu Gly Phe Thr Leu Asp
225                 230                 235                 240

Asn Thr Glu Lys Glu Lys Gln Leu Lys Ala Trp Glu Trp Arg Tyr Arg
                245                 250                 255

Leu Tyr Arg Arg Met Lys Thr Gly Phe Glu His Ala Arg Ala Pro Glu
            260                 265                 270

Met Pro Thr Asn Val Cys Leu Met Val Thr Ser Ser Thr Ser Leu Thr
            275                 280                 285

Val Ser Phe Gln Glu Pro Leu Ser Val Asn Ala Ala Val Val Thr Arg
    290                 295                 300

Tyr Lys Val Glu Trp Ser Met Ser Glu Asp Phe Ser Pro Leu Ala Gly
305                 310                 315                 320

Glu Ile Ile Met Asp Asn Leu Gln Thr Leu Arg Cys Thr Ile Thr Gly
            325                 330                 335

Leu Thr Met Gly Gln Gln Tyr Phe Val Gln Val Ser Ala Tyr Asn Met
            340                 345                 350

Lys Gly Trp Gly Pro Ala Gln Thr Thr Thr Pro Ala Cys Ala Ser Pro
            355                 360                 365

Ser Asn Trp Lys Asp Tyr Asp Asp Arg Glu Pro Arg His Lys Gly Gln
    370                 375                 380

Ser Glu Val Leu Glu Gly Leu Leu Gln Gln Val Arg Ala Leu His Gln
385                 390                 395                 400

His Tyr Ser Cys Arg Glu Ser Thr Lys Leu Gln Thr Thr Gly Arg Lys
                405                 410                 415

Gln Ser Val Ser Arg Ser Leu Lys His Leu Phe His Ser Ser Asn Lys
            420                 425                 430

Phe Val Lys Thr Leu Lys Arg Gly Leu Tyr Ile Ala Val Ile Phe Tyr
            435                 440                 445

Tyr Lys Asp Asn Ile Leu Val Thr Asn Glu Asp Gln Val Pro Ile Val
    450                 455                 460

Glu Ile Asp Asp Ser His Thr Ser Ser Ile Thr Gln Asp Phe Leu Trp
465                 470                 475                 480

Phe Thr Lys Leu Ser Cys Met Trp Glu Asp Ile Arg Trp Leu Arg Gln
                485                 490                 495

Ser Ile Pro Ile Ser Ser Ser Ser Thr Val Leu Gln Thr Arg Gln
            500                 505                 510

Lys Met Leu Ala Ala Thr Ala Gln Leu Gln Asn Leu Leu Gly Thr His
            515                 520                 525

Asn Leu Gly Arg Val Tyr Tyr Glu Pro Ile Lys Asp Arg His Gly Asn
    530                 535                 540

Ile Leu Ile Val Thr Ile Arg Glu Val Glu Met Leu Tyr Ser Phe Phe
545                 550                 555                 560

Asn Gly Lys Trp Met Gln Ile Ser Lys Leu Gln Ser Gln Arg Lys Ser
                565                 570                 575

Leu Ser Thr Pro Glu Glu Pro Thr Ala Leu Asp Ile Leu Leu Ile Thr
```

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            580                 585                 590
Ile Gln Asp Ile Leu Ser Tyr His Lys Arg Ser His Gln Arg Leu Phe
            595                 600                 605
Pro Gly Leu Tyr Leu Gly Tyr Leu Lys Leu Cys Ser Ser Val Asp Gln
            610                 615                 620
Ile Lys Val Leu Val Thr Gln Lys Leu Pro Asn Ile Leu Cys His Val
625                 630                 635                 640
Lys Ile Arg Glu Asn Asn Asn Ile Ser Arg Glu Glu Trp Glu Trp Ile
                    645                 650                 655
Gln Lys Leu Ser Gly Ser Glu Ser Met Glu Ser Val Asp His Thr Ser
                    660                 665                 670
Asp Cys Pro Met Gln Leu Phe Phe Tyr Glu Leu Gln Met Ala Val Lys
                    675                 680                 685
Ala Leu Leu Gln Gln Ile Asn Ile Pro Leu His Gln Ala Arg Asn Phe
            690                 695                 700
Arg Leu Tyr Thr Gln Glu Val Leu Glu Met Gly His Asn Val Ser Phe
705                 710                 715                 720
Leu Leu Leu Leu Pro Ala Ser Asp Asp Val Cys Thr Ala Pro Gly Gln
                    725                 730                 735
Asn Asn Pro Tyr Thr Pro His Ser Gly Phe Leu Asn Leu Pro Leu Gln
                    740                 745                 750
Met Phe Glu Leu Gly Ile Val Ala Cys Phe Thr
            755                 760
```

```
<210> SEQ ID NO 551
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 551

agctctgtag ctctgtggat c                                          21


<210> SEQ ID NO 552
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 552

aggcggaagt tccttgcctg g                                          21


<210> SEQ ID NO 553
<211> LENGTH: 2281
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 553

gcgggccgca gccagcgcac ccagaccctg cgctgccctc ggacggccgg gcgcggagcc      60

ccagctgcgg aggccgacgg cacccggccc cgagcgcctc gacgccgagc cgcgcgcgcc     120

ttctccgcca ggcccggcgg gcgggagcgg gggcgaggga gcaggagcgg ccagtgcccc     180

cgacacccc ggcccggcac ccccggcccg gcatcccccg ccgccgccgc cgccgcctca     240

aggccgcccg ctccccgcag gtggacgcgg ccatgggccg aggggtgcgc gtgctgctgc     300
```

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```
tgctgagcct gctgcactgc gccggggggca gcgagggcag gaagacctgg cggcgccggg      360

gtcagcagcc gcctcctccc ccgcggaccg aggcggcgcc ggcggccgga cagcccgtgg      420

agagcttccc gctggacttc acggccgtgg agggtaacat ggacagcttc atggcgcaag      480

tcaagagcct ggcgcagtcc ctgtacccct gctccgcgca gcagctcaac gaggacctgc      540

gcctgcacct cctactcaac acctcggtga cctgcaacga cggcagcccc gccggctact      600

acctgaagga gtccaggggc agccggcggt ggctcctctt cctggaaggc ggctggtact      660

gcttcaaccg cgagaactgc gactccagat acgacaccat gcggcgcctc atgagctccc      720

gggactggcc gcgcactcgc acaggcacag ggatcctgtc ctcacagccg gaggagaacc      780

cctactggtg gaacgcaaac atggtcttca tccctactg ctccagtgat gtttggagcg       840

gggcttcatc caagtctgag aagaacgagt acgccttcat gggcgccctc atcatccagg      900

aggtggtgcg ggagcttctg ggcagagggc tgagcggggc caaggtgctg ctgctggccg      960

ggagcagcgc gggggggcacc ggggtgctcc tgaatgtgga ccgtgtggct gagcagctgg     1020

agaagctggg ctacccagcc atccaggtgc gaggcctggc tgactccggc tggttcctgg     1080

acaacaagca gtatcgccac acagactgcg tcgacacgat cacgtgcgcg cccacggagg     1140

ccatccgccg tggcatcagg tactggaacg gggtggtccc ggagcgctgc cgacgccagt     1200

tccaggaggg cgaggagtgg aactgcttct ttggctacaa ggtctacccg accctgcgct     1260

gccctgtgtt cgtggtgcag tggctgtttg acgaggcaca gctgacggtg gacaacgtgc     1320

acctgacggg gcagccggtg caggaggggcc tgcggctgta catccagaac ctcggccgcg     1380

agctgcgcca cacactcaag gacgtgccgg ccagctttgc ccccgcctgc ctctcccatg     1440

agatcatcat ccggagccac tggacggatg tccaggtgaa ggggacgtcg ctgccccgag     1500

cactgcactg ctgggacagg agcctccatg acagccacaa ggccagcaag accccccctca    1560

agggctgccc cgtccacctg gtggacagct gccctggcc ccactgcaac ccctcatgcc      1620

ccaccgtccg agaccagttc acggggcaag agatgaacgt ggcccagttc ctcatgcaca     1680

tgggcttcga catgcagacg gtggcccagc cgcagggact ggagcccagt gagctgctgg     1740

ggatgctgag caacgaaagc taggcagact gtctggagga ggagccggca ctgaggggcc     1800

cagacacccg ctgccccagt gccacctcac cccccaccag caggccctcc cgtctcttcg     1860

ggacagggcc ccagccgtcc ccctgtctg ggtctgccca ctgccctcct gccccggctt      1920

tccctgcccc tctcccacag cccagccaga gacaagggac ctgctgtcat ccccatctgt     1980

ggcctggggg tccttcctga caacgagggg gtagccagaa gagaagcact ggattcctca     2040

gtccaccagc tcagacagca cccaccggcc ccacccatca gcccttttta tattatttta     2100

taaagtgact tttttattac tttaattttt taaaaaaagg aaaataagaa tatatgatga     2160

atgatattgt tttgtaactt tttaaaaatg attttaaaga gacaaaaaag aacctcaaaa     2220

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     2280

a                                                                     2281
```

<210> SEQ ID NO 554
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 554

```
Met Gly Arg Gly Val Arg Val Leu Leu Leu Leu Ser Leu Leu His Cys
1               5                   10                  15
```

-continued

```
Ala Gly Gly Ser Glu Gly Arg Lys Thr Trp Arg Arg Arg Gly Gln Gln
             20                  25                  30

Pro Pro Pro Pro Pro Arg Thr Glu Ala Ala Pro Ala Ala Gly Gln Pro
             35                  40                  45

Val Glu Ser Phe Pro Leu Asp Phe Thr Ala Val Glu Gly Asn Met Asp
         50                  55                  60

Ser Phe Met Ala Gln Val Lys Ser Leu Ala Gln Ser Leu Tyr Pro Cys
65                  70                  75                  80

Ser Ala Gln Gln Leu Asn Glu Asp Leu Arg Leu His Leu Leu Leu Asn
                 85                  90                  95

Thr Ser Val Thr Cys Asn Asp Gly Ser Pro Ala Gly Tyr Tyr Leu Lys
                100                 105                 110

Glu Ser Arg Gly Ser Arg Arg Trp Leu Leu Phe Leu Glu Gly Gly Trp
            115                 120                 125

Tyr Cys Phe Asn Arg Glu Asn Cys Asp Ser Arg Tyr Asp Thr Met Arg
            130                 135                 140

Arg Leu Met Ser Ser Arg Asp Trp Pro Arg Thr Arg Thr Gly Thr Gly
145                 150                 155                 160

Ile Leu Ser Ser Gln Pro Glu Glu Asn Pro Tyr Trp Trp Asn Ala Asn
                165                 170                 175

Met Val Phe Ile Pro Tyr Cys Ser Ser Asp Val Trp Ser Gly Ala Ser
            180                 185                 190

Ser Lys Ser Glu Lys Asn Glu Tyr Ala Phe Met Gly Ala Leu Ile Ile
            195                 200                 205

Gln Glu Val Val Arg Glu Leu Leu Gly Arg Gly Leu Ser Gly Ala Lys
    210                 215                 220

Val Leu Leu Leu Ala Gly Ser Ser Ala Gly Gly Thr Gly Val Leu Leu
225                 230                 235                 240

Asn Val Asp Arg Val Ala Glu Gln Leu Glu Lys Leu Gly Tyr Pro Ala
                245                 250                 255

Ile Gln Val Arg Gly Leu Ala Asp Ser Gly Trp Phe Leu Asp Asn Lys
            260                 265                 270

Gln Tyr Arg His Thr Asp Cys Val Asp Thr Ile Thr Cys Ala Pro Thr
            275                 280                 285

Glu Ala Ile Arg Arg Gly Ile Arg Tyr Trp Asn Gly Val Val Pro Glu
    290                 295                 300

Arg Cys Arg Arg Gln Phe Gln Glu Gly Glu Glu Trp Asn Cys Phe Phe
305                 310                 315                 320

Gly Tyr Lys Val Tyr Pro Thr Leu Arg Cys Pro Val Phe Val Val Gln
            325                 330                 335

Trp Leu Phe Asp Glu Ala Gln Leu Thr Val Asp Asn Val His Leu Thr
            340                 345                 350

Gly Gln Pro Val Gln Glu Gly Leu Arg Leu Tyr Ile Gln Asn Leu Gly
            355                 360                 365

Arg Glu Leu Arg His Thr Leu Lys Asp Val Pro Ala Ser Phe Ala Pro
    370                 375                 380

Ala Cys Leu Ser His Glu Ile Ile Ile Arg Ser His Trp Thr Asp Val
385                 390                 395                 400

Gln Val Lys Gly Thr Ser Leu Pro Arg Ala Leu His Cys Trp Asp Arg
            405                 410                 415

Ser Leu His Asp Ser His Lys Ala Ser Lys Thr Pro Leu Lys Gly Cys
            420                 425                 430

Pro Val His Leu Val Asp Ser Cys Pro Trp Pro His Cys Asn Pro Ser
```

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```
         435              440              445
Cys Pro Thr Val Arg Asp Gln Phe Thr Gly Gln Glu Met Asn Val Ala
   450                      455              460

Gln Phe Leu Met His Met Gly Phe Asp Met Gln Thr Val Ala Gln Pro
465                  470              475                  480

Gln Gly Leu Glu Pro Ser Glu Leu Leu Gly Met Leu Ser Asn Gly Ser
             485              490                  495
```

```
<210> SEQ ID NO 555
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 555

gagatcatca tccggagcca c                                           21


<210> SEQ ID NO 556
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 556

tagcttccgt tgctcagcat c                                           21


<210> SEQ ID NO 557
<211> LENGTH: 522
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 557

atgtaagcaa agtagtcatt aaaaatacac cctctacttg ggctttatac tgcatacaaa     60

tttactcatg agccttcctt tgaggaagga tgtggatctc caaataaaga tttagtgttt    120

attttgagct ctgcatctta acaagatgat ctgaacacct ctcctttgta tcaataaata    180

gccctgttat tctgaagtga gaggaccaag tatagtaaaa tgctgacatc taaaactaaa    240

taaatagaaa acaccaggcc agaactatag tcatactcac acaaagggag aaatttaaac    300

tcgaaccaag caaaaggctt cacggaaata gcatggaaaa acaatgcttc cagtggccac    360

ttcctaagga ggaacaaccc cgtctgatct cagaattggc accacgtgag cttgctaagt    420

gataatatct gtttctacta cggatttagg caacaggacc tgtacattgt cacattgcat    480

tattttctt caagcgttaa taaaagtttt aaataaatgg ca                       522


<210> SEQ ID NO 558
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 558

actacggatt taggcaacag g                                           21


<210> SEQ ID NO 559
<211> LENGTH: 24
```

```
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 559

gagatctcga gatctcgatc gtac                                          24


<210> SEQ ID NO 560
<211> LENGTH: 2383
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 560

cttttctctt gttgagtgca aatggagaac agctgctcac gctcgtcgtc tgacatcagc    60

tatttctcag gatgaccctg cgagacaggc cagggtcatt agacccaatt tggttctcag   120

caaatatgtg tttattcctg catgcgtggg ccacaggctg gtttcttggg tgcaatgaat   180

agctgcaggt ttattagggt gtcttttag atggatgtat gtttcccgat gtctatagaa    240

cactccggac cccggagagt gaagactctg cctgtcggac ttgctttgag aagatccttc   300

tccacctccc catggcagaa gttgcttcac agaggggaac agttttatgg atgtggctga   360

gaccttaaac ttgaggcaac ccatctgagg tggcatccag aggagactgg ctggcccctc   420

cttcaccttg gatgtagtgc tgtttctagg atctctttc aatcagcaaa acaggggatg    480

ttccaagagg gtgtggattc cctgccatcc cacatggtca agtggagggg acgggaaaaa   540

gctatgaagg gtttgtgacc acacagactc tcctggcccc ctgtcctttt ggaaagaaga   600

cagggatgaa atataatcaa gcaattaacc accccatca tcaccaagaa caacagtatc    660

aacaagaaga cagggacaa caaaacccac ggatgaaaca ttcctttctc agctcagatc    720

ttatctggtg cgttctctct ctgctctgtc ttggtgtgtg gtttagagaa acatggacaa   780

cgctgtttgg aagaacaggt gagcgagggt ggggaatttc agaggcctgg gcccaccgcc   840

tccacccctt ccccagttta acctttgaca ggatcttcac ctctctctga tcagcattgc   900

ttcttgttca aaggcctcag ccacccagct gtgtcccttt ccccagaaag caagggcaga   960

tggcagtggg tctgttgatg agagaacttt aagggcccaa tcagtccctg ggcacccct   1020

cctgggctcg ttttctccag gaggctgcat tctgatccat aaaccttctc ctcggggttt   1080

agggtcgagc tgttcctgat gtttatcgga gactgggatc aaagctatcc aggtcataaa   1140

tctctctctg tggctgttgg ccccagggc agctgaagag ggttgacagc cctttggacc   1200

tcaaaggaaa aaatgtgctc tactccaccc actcccagct ctgccaagaa gctgtcctct   1260

gagaagccat ggctgggccg ttccattctg gggagctgct gaaaagagct gggaggccga   1320

gaagaacttg cgtgtgctgg gggagaggaa gcctggcctt gagggagggg tgcaggtgtg   1380

gctcctctgt gtgtgggggc tggggacct tgtgtgcctt ttccttgtgg ctgtgaaatg   1440

ctttatgagt acttccatag gaggatggac agggagtcgg ggagataaac tcagccacaa   1500

ggccccaggg cctcaggaaa cttgcaccca accctctcat tttacagaag aaaactgtgc   1560

ctggaaggtt gaagggtttg ttcccagtca cacaaccagg gatccttagg acagccagac   1620

caggaaacca tttccaaact gccaagccat ggcagagtat caagacctca ggaaccatcg   1680

agacaccatg gaagcattgg gaaaagcctc cttagctttt gaagctcctc attgttcttg   1740

agtgtgcatg gagcccatga ctgcgggggtt ttgtagacac ctcagggatt acatgactgg   1800

tacccctgac aaagtcaagg ctgctggaca aaatgagtcc gaggatttca ggggcagctg   1860
```

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```
ggcgcaggag ctggtgggct gttgggagtg ccccttact gggcaggctt ccttcctcct      1920

ggtgatgggg ggttcctcag cacaaaagtg aaggggtgga ggggctggag gagcaggaat      1980

ctctcttgtt gataggtatg aggccttgaa gtcctttct ttgtcccagg attcatggac      2040

gcttcggggc tgatctttga gttttcaagc atggggtgca gagacgttta ggtaaactct      2100

taccgtcctc tctcttcgtc agggcttccc aggaatcaac aatgcccaag aaggaaggga      2160

ttgtagaaat agcttaaccc tttcatttac caacgtggaa attgaagccc agggaaggga      2220

agggaccggt cgtggaaggg agagccatca gcagaaagag accctgagat cttcgcctgg      2280

gattcccagg aagtccagcc cgagctgatt cacagaacaa atgcatgcaa accttgctat      2340

caataaatta cacatgcact tacgtaaaaa aaaaaaaaaa aaa                        2383
```

```
<210> SEQ ID NO 561
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 561

cagagacgtt taggtaaact c                                                21
```

```
<210> SEQ ID NO 562
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 562

taccaacgtg gaaattgaag c                                                21
```

```
<210> SEQ ID NO 563
<211> LENGTH: 2336
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 563

aaaaaaacct atctaaggag gagccaagat ggccgcatag gaacagctcc agtccacagc       60

tcccagcgtg agcgacgcag aagacgggtg atttctgcat ttccatctga ggtaccgggt      120

tcttctcact agggagttcc agacagtggg cgcagcaggc ttttcttctt ggagctgaaa      180

caggcgcact ggcgagggtt gtgaggaaag gtttgcagcc ccctgccttg gtctgctata      240

gccagtgaca cgatcaatac cagggtgagc agcagaggaa gctcagggaa gattatgaag      300

atgagaattc attacctatc aaagaaaatg cgtaaactct agaagtattg cttgctcctt      360

tgccacaaag tgtacattca agagtaaatt gtttaaagcc aaagggcctt gcgccacgtc      420

cttagcctca gctttctact tgctaaaatg gaaataacaa cagtacctac cttacagacc      480

tggcgtgagg attaaattat accagcaaag tgcctggcac ctagaatttg cctgagttct      540

gatcaatgct aaaaacacca tttaacagtg cccttcctg cctgggaagc ccacaaagat      600

ttcgcttttc acttattact catcaaactg actctggttc acagtggaaa agagaagaaa      660

agctgatgga gaaatggcag tgaagaagga gaacaaaatg tcagagcaat acttttgagc      720

gacttatcct ctgttctgca atatttgcaa aagtcagtct atagacgtga agccaacagg      780
```

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```
gaccctcagg cctgtgcatc aggatggtgg gctgcctaag tcctctgggg acagcagtgc      840

cagaaggagt attggacaca gtgacccgac tgtatgagat gagaaaaaac aaaaacagga      900

ggtccgcagt actgatgaac taatctgtca ctcacaagct caggtctgca aaaaaaagaa      960

acgaagcact aaacatggcc ataagagatg gaaatgcaag tcttcatttc taaatgataa     1020

tcaaaccaac gatcagaaac tgattaactg tgtaattgaa ttgaattgaa aatcatccca     1080

tgaataacaa tccatcctac cttcaagggg ttaggaagct aactacaggt aattgctatc     1140

agaaatctga tttgatttcc aaaaattgtg tgaatgaacc aagtttcttc atcttgatat     1200

actaggcagg gagtttgttc ttccaagtac tagactgctt aattgcttgc ttgggggagg     1260

agaaatccta ggggaaaggc atatatgagc aatttctact ctgtgaagcc agcgctgtgt     1320

cctgagctgg atcatggcca gaaacagaaa agtctactct tccctacagt ggaagcaact     1380

gtggatattt catcctagga gtgaatgaaa aaacctaaag ctcatacttc atgggaatct     1440

ttcaatattc tgactgaaaa ctggttattt gctcctccaa cccaaagcca tctaggaaca     1500

gcactcagaa caggaaaaaa aaaagacaaa aataataatt attccaaaac gtatttgagc     1560

agaaacaaac acaaacattt gcattattaa atgggcttgt tcacacctgc tgagtagata     1620

taagacgata tttaagacaa gagctaaaaa ataaaccatc cctttctggt tttgagtgac     1680

agcagagcaa taaaaattat tttcacattc ttttccctat tgttagaagt aatcatttga     1740

gtaaatacac ttatctgtgc tgtaactatt gaaatgaatc cacttcaaat atgtatacca     1800

cctttctttt ttatatttct agatatggtt tcaatataga ctttctgact tttatggtat     1860

acatatagga caatattcta ttcttctttc ctttttaaata cttactgttt caatttcaaa     1920

taaaaaatca gcattctagt ttgtacattt tagcacagaa atgtttacaa ccttcagcac     1980

aattgctttt gtaatttact gacttggcat tttgaggcgt ttttaacaaa ttatgagaaa     2040

taacaccttc agaaagcatg tgactacttt gatgcaacta tttacaatgt attcataaga     2100

agtcattaac ctgtagagtt cttagacatg tggaaccttt aacaattata ctaaagagta     2160

catacaaaat acagagctat gtaataataa ctaattttaa atcctgacaa attagaagtt     2220

aagcctacta tctgtaaaaa tatgtcctga ttcattttt taagtatata cctgagcctt      2280

taaaaagtat atgcctttac aattgatttc caataaacaa tactgaataa catact          2336
```

```
<210> SEQ ID NO 564
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 564

gcaatacttt tgagcgactt atcc                                               24


<210> SEQ ID NO 565
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 565

gatagcaatt acctgtagtt agc                                                23
```

```
<210> SEQ ID NO 566
<211> LENGTH: 1187
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 566

gaacaacatg gcttcccca gcgtgagact cgcttgtcct cccaccgcct gctctctcct        60

gatgaccagg ttccaggagt tatcaaagaa cagcctctga gctgcgtgga gaaagccatg       120

gagacagcca aagaaaacg gcaggattag attaacctgt gattcctggc tggccacgag       180

gtcacccatg gcatggagct gcccacaacg cccttctcag catgaagcat cctgaaagat       240

ccagggccag gttccccagg attggggagt tggaagctca ttggcactgt caaatttgaa       300

gaagaggcgt gctctgactg cctggacagg acccggaatc aaaccgcagg ccctgggtca       360

ccgctgccgg aaagagccag ttcctgtccg tccatgcacc caccaccaaa acccaggcct       420

tcctggaggt gctaggggag gccatgcccc ttttctgagt gcttggaagt gactgctgca       480

agtgacaagt gaccacgcct tttccccgc gggtataaat tcagaggcgc tgcgctccga       540

ttctggcagt gcagctgtgg gaacctctcc acgcgcacga actcagccaa cgatttctga       600

tagattttg ggagtttgac cagagatgca aggggtgaag gagcgcttcc taccgttagg       660

gaactctggg gacagagcgc cccggccgcc tgatggccga ggcagggtgc gacccaggac       720

ccaggacggc gtcgggaacc ataccatggc ccggatcccc aagaccctaa agttcgtcgt       780

cgtcatcgtc gcggtcctgc tgccagtgag tccccgccgc ggtccctggc tggggaagag       840

cgcacctggc gccgggaggg ggcagggaga cggggacacg gcagggatgc ctggccctgg       900

tcacctgcgg ccgggcatgt ccgggcagga cgaactcgcc gtcggagtca ggggaagaac       960

tgggtcccg ggctgggcag gagggacccg gccgcgaggg agcagagagg cggtcccct      1020

ggctgccccg agcccgcgaa gggagggaag ttccagaatc gagagaggga gggagtcaag     1080

gtggaaccca tagagtgagc ctcctgaaga cacagagcgg ttgcctctct cattaattaa     1140

ttaattagtt aataaaatta accccatgtt taaaaaaaa aaaaaaa                  1187


<210> SEQ ID NO 567
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 567

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
1               5                   10                  15

Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
            20                  25                  30

Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
        35                  40                  45

Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Ser Pro Arg
    50                  55                  60

Arg Gly Pro Trp Leu Gly Lys Ser Ala Pro Gly Ala Gly Arg Gly Gln
65                  70                  75                  80

Gly Asp Gly Asp Thr Ala Gly Met Pro Gly Pro Gly His Leu Arg Pro
                85                  90                  95

Gly Met Ser Gly Gln Asp Glu Leu Ala Val Gly Val Arg Gly Arg Thr
            100                 105                 110

Gly Ser Pro Gly Trp Ala Gly Gly Thr Arg Pro Arg Gly Ser Arg Glu
        115                 120                 125
```

```
Ala Val Pro Leu Ala Ala Pro Ser Pro Arg Arg Glu Gly Ser Ser Arg
    130                 135                 140

Ile Glu Arg Gly Arg Glu Ser Arg Trp Asn Pro
145                 150                 155


<210> SEQ ID NO 568
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 568

ggattgggga gttggaagct c                                          21


<210> SEQ ID NO 569
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 569

agaaatcgtt ggctgagttc g                                          21


<210> SEQ ID NO 570
<211> LENGTH: 857
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 570

catccctctg ctccagagc tcagagccac ccacagccgc agccatgctg tgcctcctgc    60

tcaccctggg cgtggccctg gtctgtggtg tcccggccat ggacatcccc cagaccaagc   120

aggacctgga gctcccaaag ttggcaggga cctggcactc catggccatg gcgaccaaca   180

acatctccct catggcgaca ctgaaggccc ctctgagggt ccacatcacc tcactgttgc   240

ccacccccga ggacaacctg gagatcgttc tgcacagatg ggagaacaac agctgtgttg   300

agaagaaggt ccttggagag aagactgaga atccaaagaa gttcaagatc aactatacgg   360

tggcgaacga ggccacgctg ctcgatactg actacgacaa tttcctgttt ctctgcctac   420

aggacaccac caccccatc cagagcatga tgtgccagta cctggccaga gtcctggtgg   480

aggacgatga gatcatgcag ggattcatca gggctttcag gcccctgccc aggcacctat   540

ggtacttgct ggacttgaaa cagatggaag agccgtgccg tttctaggtg agctcctgcc   600

tggtcctgcc tcctggctca cctccgcctc caggaagacc agactcccac ccttccacac   660

ctccagagca gtgggacttc ctcctgccct ttcaaagaat aaccacagct cagaagacga   720

tgacgtggtc atctgtgtcg ccatccctt cctgctgcac acctgcacca cggccatggg   780

gaggctgctc cctgggggca gagtctctgg cagaggttat taataaaccc ttggagcatg   840

aaaaaaaaaa aaaaaaa                                                 857


<210> SEQ ID NO 571
<211> LENGTH: 180
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 571

Met Leu Cys Leu Leu Leu Thr Leu Gly Val Ala Leu Val Cys Gly Val
```

-continued

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1              5              10             15

Pro Ala Met Asp Ile Pro Gln Thr Lys Gln Asp Leu Glu Leu Pro Lys
            20             25             30

Leu Ala Gly Thr Trp His Ser Met Ala Met Ala Thr Asn Asn Ile Ser
        35             40             45

Leu Met Ala Thr Leu Lys Ala Pro Leu Arg Val His Ile Thr Ser Leu
    50             55             60

Leu Pro Thr Pro Glu Asp Asn Leu Glu Ile Val Leu His Arg Trp Glu
65             70             75             80

Asn Asn Ser Cys Val Glu Lys Lys Val Leu Gly Glu Lys Thr Glu Asn
                85             90             95

Pro Lys Lys Phe Lys Ile Asn Tyr Thr Val Ala Asn Glu Ala Thr Leu
            100            105            110

Leu Asp Thr Asp Tyr Asp Asn Phe Leu Phe Leu Cys Leu Gln Asp Thr
            115            120            125

Thr Thr Pro Ile Gln Ser Met Met Cys Gln Tyr Leu Ala Arg Val Leu
    130            135            140

Val Glu Asp Asp Glu Ile Met Gln Gly Phe Ile Arg Ala Phe Arg Pro
145            150            155            160

Leu Pro Arg His Leu Trp Tyr Leu Leu Asp Leu Lys Gln Met Glu Glu
            165            170            175

Pro Cys Arg Phe
            180


<210> SEQ ID NO 572
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 572

agttcaagat caactatacg g                                           21


<210> SEQ ID NO 573
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 573

tagaaacggc acggctcttc c                                           21


<210> SEQ ID NO 574
<211> LENGTH: 4415
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 574

agagaagcaa catctttaag gtactgaggg caggagaagt taatgtagaa tactatgcca     60

gaaaaaataa attcccaaaa gtggaagtga ataaggaca tttagagatg tacaaaagct    120

gaccgaattc actaccagtc aacccacact acaagaaaca tcaaatgagt cctccaagca    180

gaaggaaccc aataccagat gaaaatccag atctccacga ggaaatgaag aacaccagaa    240

atggatcggc cctttcttca aataagagca gttggaataa caaagctgtt cagttgtacc    300
```

```
cttggaatcc actgaaatcc tgggtaggga agctccagta ccaccaactg gaaagactgg     360

gaatgcctaa tagctggtac tggccattgt cgtaggcttt gtccactctg acaaactgaa     420

gatggggact cgactcacct tcgccagcca caggaggacc tccagacgag gttaggtcga     480

cttcccgata actttagatc ctgaaacctc acgggatttt tcttctcttc cctttgatct     540

ctcttccgct tgctcaacag gacaggactc gctgcctttc tttcccgtca gaaagggatc     600

ccttgcggac aggacctaag tgagtagctg gtttccccta cttgtccttc cgggcctggg     660

tgtctcggga gctcaggctg acgggagacc taactaccgg cgagtgagac cagcaggagc     720

ctggaggggc gcgcaccagg gtggaggttt ggtgccgggg gttgagaaca acagtcaaac     780

cctcttcttc ccctggcacc acgcacctgc cccccgggac gccgaacgaa gtggtcccta     840

aagctcctct gcaggcccaa ccgaaacagg cctgaagctc caggatgggc gagaggatcc     900

tctttgagcg aaaccagcct tctgcctggc tggccctggt caacaccctg ggaagaggcc     960

gatttggcgg acagaacgga agaaaagacc taaaggtaga atctcatgat gtcgagatgt    1020

taaaacactc aaattttaag gttcgactgt gaggggggaga taggggggtct cgagcaggat    1080

cgacccctga gccttcatct gcagagtcct gtgcaccagc tcagaggaca ggactatgtg    1140

caccaatggt tctcatcagg cggcaacttc accctcacat gcctccccca tccctgctgg    1200

tacacaagac cacgactagg ggaagcccgg agggagaatg ttaacccctg gcatctatct    1260

agtcagcaga ggtgagggat gctgctaaac accttacaat ccaccggagg acacccgccc    1320

ccaccgaccc cgaagtagcc attccctgga ggtgggggaaa ctcgcctgta gatcaatgcc    1380

cacgcacttg gcggacagga aatcacgaat tggccactaa ctggatcttg gatctgagga    1440

aaaaattcca gcgtcagagg gaactctcgg agatttgccc agagcataag gaacgtactc    1500

cttccctcag tgatggatca tcacatctgg gggaaatcat agacaatttc ttttgtaggg    1560

cgaactctgc tatacagttt atgatgtcag agtgaatact ttctttgagt tgcagtcaga    1620

aactgtagat ttttaaaaat ttaaaattca ttattctctg tcagtatttc aaagtgtata    1680

cagaaagcta ttgcactgtt caggagatgg cgcctaacat tttggaaatt caaggtgatg    1740

aatgtccaga taagactatc tctcctggta caaagtttga caatgctgaa cattttttaaa    1800

ggttcttttt gatatacaaa gtgcaccaat gagtgctttt taattcttac aataattctg    1860

ggtgaggtag gtattttttcc aattcccatt ttatgcttcg gtagcccttt gtatttatac    1920

ttcaaaacac ttggctctct tgtaattatt taagaaatta gttgtgatta tttgtttaat    1980

gtgcaggagt tacaaaaggc aagcgttaga acaagacaga cctggttatg attcctggct    2040

ctgaaagctg tacaccctgt gaccctagac aggtgtttta atgcctcgct gcctctgttt    2100

cttgctctgt aaaatgtgaa caataacagt attggcctca tgcttttttt gggtttttaaa    2160

agtaataatg tggacaaaga tcagtggagt gcctggcatg ctgaacccat tccatgactg    2220

atagctatag ttgttatgat ttgtatcaat ccattttcac actgctataa ggaactacct    2280

gagactgggt aatctatgaa gaaaagaggt ttaattgact cacagttctg catggctggg    2340

agtcctcagg aacttacaat catggcagaa ggggaagcaa gacatttctt atatggcagc    2400

aggacagaaa gagagagagt gaaggggggaa gtgccacaca cttccaaaca accatatctt    2460

gtggttaatt aaaaagtact cattggtgtg ccttgtatag aaaaaaatat acactcacta    2520

tcatgagaac agcaaggagg gagtctgccc ccaaggttca atcacctccc agtagacccc    2580

tcccctgaca tgtgggggatt acaattcaag atgagatttg ggtgggggaaa cagagtcaaa    2640

ccatatcgtg attgttctat aataaagaga tgcccacatg tgtttcatca gggacagtgc    2700
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```
tcattaacca gttgtcctgc cgtaattatt aatagtatcc cctttgcttt caaaagtgtc          2760

ctagtttaca aaaagtatag aaatggagga cagaatagtg gttgcccaag attggaaaag          2820

ggtaagggta aagggtgcag aggtggatgt ggttataaaa ggcaacatgg gagatcctcg          2880

tagtgaagga accgtttagt atctccactg tggtggtaga tacccgaacc taaacatgtg          2940

aaaaattgca tgaaactaaa cacacacacc aacaagtaca agttaagtta ggaaaatcca          3000

aataagattt ctacattgta tcaataggta tatcttgatt atgatattgc aagatggtac          3060

tattcaagga aactgggtag aggctacatg agactcccct gtattatttc ctataactcc          3120

atgtgaatct acaaggatct caggattaag gaagatatcc tagtttggaa gataaaaaat          3180

atatcccagt agtaatatcc actgtcccac cagggcctga ctaccttcta taaaaagaag          3240

tgcctttgtt cccctcaagt tcctttattt ggtttattc ttcttcacag tacctacctc           3300

cacttggcag attacattta tttttcatc tttcaacagc tatttactga atgcctacta           3360

gatgccaggc ttgagatcta gcaatgaaca agatctctgt gaaacttaca ttccaggagg          3420

agaaataaat aataaaccaa aaatataatc agtaaattat ttaatatgct gggaaacaat          3480

atgtgtaatg gaagaaatat gtaaagtgat ggattagggt tctccagaga aacagaacca          3540

acaattgact catgtgatta tggaggctga gaagtctcaa gatcacagtt ggcaagcttg          3600

agacacagga gagcccatgg tgtgtttctg atttgagtcc aaaggcctga gaaccaggag          3660

agatgatggt gtgattacag ttcaaaagct ggcaggcttg aggcccagga gagccagtg           3720

ttgcagttca attccaaagg caggaaaagg ctgatatctt agctgaagca atcaggcaga          3780

aggagctctc tcttactcat gggcaggtca gacttttggt tctattcagg cctttaagtg          3840

attggatgag gatcatctac tgtggaaaga aataagcttt attcagtgta ctgattcaaa          3900

tgttaatctc atccaaaacc atgctcacag acacacccag cataatgttt gaccaagtat          3960

ctgggcacct tgtggttcag tcaaattaac acatattaac taccttagca agatgaaaag          4020

cagtgaatgc aggatggtgg ttgaaatttt aaatacgttg gttatatagt ctcattgaaa          4080

aaggaacatt tgagtgaaga cttgaagggg tggtggaata aaccatttat ttgcttattg          4140

cctgtctccc tctatcagaa tgaaagcttc atgaagcgag agacttaatt tttatctgtt          4200

atatccctag tgcctggtgc agggtaagta ctcaaaaata tttgttgagt gaataagtaa          4260

tgattgagga tggggactgg tttgtatctg gttatatctc ttgtccttag cacagtacct          4320

ggcacatcct aagccatcca aaagagttgg ttatatgatt gtctttgaat tctatgactg          4380

tttataatat acagtaaact tcactgaaga cactg                                     4415
```

```
<210> SEQ ID NO 575
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 575

gaagaacacc agaaatggat cg                                                      22


<210> SEQ ID NO 576
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
```

Oligonucleotide

<400> SEQUENCE: 576

cttcagtttg tcagagtgga c   21

<210> SEQ ID NO 577
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 577

tgtcagcttt gtctgtgcct cgcaaatcag aggcaaggga gaggttgtta ccaggggaca   60

ctgagaatgt acatttgatc tgccccagcc acggaagtca gagtaggatg cacagtacaa   120

aggaggggg agtggaggcc tgagagggaa gtttctggag ttcagatact ctctgttggg   180

aacaggacat ctcaacagtc tcaggttcga tcagtgggtc ttttggcact ttgaaccttg   240

accacaggga ccaagaagtg gcaatgagga cacctgcagg aggggctagc ctgactccca   300

gaactttaag actttctccc cactgccttc tgctgcagcc caagcaggga gtgtccccct   360

cccagaagca tatcccagat gagtggtaca ttatataagg attttttta agttgaaaac   420

aactttcttt tcttttgta tgatggtttt ttaacccagt cattaaaaat gtttataaat   480

caaa   484

<210> SEQ ID NO 578
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
     Oligonucleotide

<400> SEQUENCE: 578

cagccacgga agtcagagta g   21

<210> SEQ ID NO 579
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
     Oligonucleotide

<400> SEQUENCE: 579

ccactcatct gggatatgct tctg   24

<210> SEQ ID NO 580
<211> LENGTH: 592
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (62)..(62)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 580

ggtgcatgtt cattgggcat cttccattcg acccctttgc ccacgtggtg accgctgggg   60

anctgtgaga gtgtgagggg cacgttccag ccgtctggac tctttctctc ctactgagac   120

gcagcctata ggtccgcagg ccagtcctcc caggaactga aatagtgaaa tatgagttgg   180

cgaggaagat caacatatag gcctaggcca agaagaagtt tacagcctcc tgagctgatt   240

ggggctatgc ttgaacccac tgatgaagag cctaaagaag agaaaccacc cactaaaagt   300

```
cggaatccta cacctgatca gaagagagaa gatgatcagg gtgcagctga gattcaagtg     360

cctgacctgg aagccgatct ccaggagcta tgtcagacaa agactgggga tggatgtgaa     420

ggtggtactg atgtcaaggg gaagattcta ccaaaagcag agcactttaa aatgccagaa     480

gcaggtgaag ggaaatcaca ggtttaaagg aagataagct gaaacaacac aaactgtttt     540

tatattagat attttacttt aaaatatctt aataaagttt taagcttttc tc             592
```

<210> SEQ ID NO 581
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 581

```
attggggcta tgcttgaacc c                                               21
```

<210> SEQ ID NO 582
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 582

```
tttcccttca cctgcttctg g                                               21
```

<210> SEQ ID NO 583
<211> LENGTH: 2514
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 583

```
actggggtct tctccatgcg gctcgggcta tgacagcctc cgtgctcctc caccccgct      60

ggatcgagcc caccgtcatg tttctctacg acaacggcgg cggcctggtg gccgacgagc     120

tcaacaagaa catggaaggg gcggcggcgg ctgcagcagc ggctgcagcg gcggcggctg     180

ccggggccgg gggcgggggc ttcccccacc cggcggctgc ggcggcaggg ggcaacttct     240

cggtggcggc ggcggccgcg gctgcggcgg cggccgcgcg gcgcggctg caaccagtgc     300

tggcgcaccc ggcgcgcctt gcgccaggag ccgcgtccgc ctacagcagc gcccccgggg     360

aggcgccccc gtcggctgcc gccgctgctg ccgcggctgc cgctgcagcc gccgccgccg     420

ccgccgcgtc gtcctcggga ggtcccggcc cggcgggccc ggcgggcgca gaggccgcca     480

agcaatgcag cccctgctcg gcagcggcgc agagctcgtc ggggcccgcg gcgctgccct     540

atggctactt cggcagcggc tactacccgt gcgcccgcat gggcccgcac cccaacgcca     600

tcaagtcgtg cgcgcagccc gcctcggccg ccgccgccgc cgccttcgcg gacaagtaca     660

tggataccgc cggcccagct gccgaggagt tcagctcccg cgctaaggag ttcgccttct     720

accaccaggg ctacgcagcc gggccttacc accaccatca gcccatgcct ggctacctgg     780

atatgccagt ggtgccgggc ctcggggccc ccggcgagtc gcgccacgaa cccttgggtc     840

ttcccatgga aagctaccag ccctgggcgc tgcccaacgg ctggaacggc caaatgtact     900

gccccaaaga gcaggcgcag cctcccacc tctggaagtc cactctgccc gacgtggtct     960

cccatccctc ggatgccagc tcctatagga gggggagaaa gaagcgcgtg ccttatacca    1020
```

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aggtgcaatt aaaagaactt gaacgggaat acgccacgaa taaattcatt actaaggaca      1080

aacggaggcg gatatcagcc acgacgaatc tctctgagcg gcaggtcaca atctggttcc      1140

agaacaggag ggttaaagag aaaaaagtca tcaacaaact gaaaaccact agttaatgga      1200

ttaaaaatag agcaagaagg caacttgaag aaacgcttca gaactcgttg ctttgcccag      1260

ataatgataa taatgcttaa taataattga agaatgggaa agagaaagag acagagactg      1320

gcattttcct ctcccgaagg agatctcttt ctctttaatg gaatctacaa ctgttttaaa      1380

actttaagaa aggtaaagac tgccagttct tccgccaacc ccatcagccc agcccgttaa      1440

atgtcaaacg tcaacccca aaatacgcaa tttcagataa gttacgcagt tactgaaatc      1500

ttgtaagtat ttaagtgatc gttacatttt aggacactgc gttagatggt aataatctgg      1560

aagttggtta caaacgcaag aggccattgt aaacatctgc ttgtccttct taggtcgcca      1620

ttccctttgc atgttaagcg tctgctcagg taaatcttag tgaaattcct accgttgttg      1680

tacgttctgc aaaacatttt atgtatagat ttagagggga aacgagaagg tactgaaata      1740

atgatcttgg aatatttgct gtgaagggag aaagggagag aaaactcttc tgaggatcat      1800

ttgtcttggt agtatagtaa aaccaaccag ctgaaccttt caggctacaa gagaacccgg      1860

gtcggtaatg tcttttttaag aataatttttt aattgcttat aacaagcata ttttgtggca      1920

tttgaactat atttactgct ccaatatccg ttattttcca aaggattttg tatctttttg      1980

aaaatgttta catcatcaga tgatccacag aattcacttt atgtgagatc tcccgagagt      2040

ttccatccca acataatgga ctttggtttg aacacaattc gttttttcat ttgaattggc      2100

atttcccaat atttgctaaa catttgctgg agaaatcatt tttcttttttt cttttttaga      2160

aaactcagaa tgaaaattca ttcccctgaa atatttaggt gtctatattc tatattttga      2220

tctattaagg gattagtatt tttccatgtt tattgtgtta tcagagtgca ttagaaagat      2280

tagtgattca tcttcacagc acatttttaa tcaagcagtt atttcaacca gcacattcgt      2340

tttgttcata ttcactatag aatgatatct tgtaaataaa gacattcagc acactgtgaa      2400

aatgtatttg tgcacctgct ttttaaatat ttctactaaa aatgaaaaaa aaaaaccctt      2460

agacctgtag atagtgatat cgtaatatta attgttaata aaatagtcac tgcc           2514
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<210> SEQ ID NO 584
<211> LENGTH: 388
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 584

Met Thr Ala Ser Val Leu Leu His Pro Arg Trp Ile Glu Pro Thr Val
1               5                   10                  15

Met Phe Leu Tyr Asp Asn Gly Gly Gly Leu Val Ala Asp Glu Leu Asn
            20                  25                  30

Lys Asn Met Glu Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
        35                  40                  45

Ala Ala Ala Gly Ala Gly Gly Gly Gly Phe Pro His Pro Ala Ala Ala
    50                  55                  60

Ala Ala Gly Gly Asn Phe Ser Val Ala Ala Ala Ala Ala Ala Ala Ala
65                  70                  75                  80

Ala Ala Ala Ala Asn Gln Cys Arg Asn Leu Met Ala His Pro Ala Pro
                85                  90                  95

Leu Ala Pro Gly Ala Ala Ser Ala Tyr Ser Ser Ala Pro Gly Glu Ala
            100                 105                 110
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Pro Pro Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
        115                 120                 125

Ala Ala Ala Ala Ala Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Pro
    130                 135                 140

Ala Gly Ala Glu Ala Ala Lys Gln Cys Ser Pro Cys Ser Ala Ala Ala
145                 150                 155                 160

Gln Ser Ser Ser Gly Pro Ala Ala Leu Pro Tyr Gly Tyr Phe Gly Ser
                165                 170                 175

Gly Tyr Tyr Pro Cys Ala Arg Met Gly Pro His Pro Asn Ala Ile Lys
            180                 185                 190

Ser Cys Ala Gln Pro Ala Ser Ala Ala Ala Ala Ala Phe Ala Asp
            195                 200                 205

Lys Tyr Met Asp Thr Ala Gly Pro Ala Ala Glu Glu Phe Ser Ser Arg
    210                 215                 220

Ala Lys Glu Phe Ala Phe Tyr His Gln Gly Tyr Ala Ala Gly Pro Tyr
225                 230                 235                 240

His His His Gln Pro Met Pro Gly Tyr Leu Asp Met Pro Val Val Pro
                245                 250                 255

Gly Leu Gly Gly Pro Gly Glu Ser Arg His Glu Pro Leu Gly Leu Pro
            260                 265                 270

Met Glu Ser Tyr Gln Pro Trp Ala Leu Pro Asn Gly Trp Asn Gly Gln
            275                 280                 285

Met Tyr Cys Pro Lys Glu Gln Ala Gln Pro Pro His Leu Trp Lys Ser
    290                 295                 300

Thr Leu Pro Asp Val Val Ser His Pro Ser Asp Ala Ser Ser Tyr Arg
305                 310                 315                 320

Arg Gly Arg Lys Lys Arg Val Pro Tyr Thr Lys Val Gln Leu Lys Glu
                325                 330                 335

Leu Glu Arg Glu Tyr Ala Thr Asn Lys Phe Ile Thr Lys Asp Lys Arg
            340                 345                 350

Arg Arg Ile Ser Ala Thr Thr Asn Leu Ser Glu Arg Gln Val Thr Ile
            355                 360                 365

Trp Phe Gln Asn Arg Arg Val Lys Glu Lys Lys Val Ile Asn Lys Leu
    370                 375                 380

Lys Thr Thr Ser
385
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<210> SEQ ID NO 585
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 585

tctggaagtc cactctgccc gacg   24

<210> SEQ ID NO 586
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 586

tgtgacctgc cgctcagaga g   21

<210> SEQ ID NO 587
<211> LENGTH: 8769
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 587

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cttctcctgg gctctccccg aactctcccg cgacctctgc gcgccctcag gccgccttcc   180

ccgccctggg ctcgggacaa cttctggggt ggggtgcaaa gaaagtttgc ggctcctgcc   240

gccggcctct ccgcctcttg gcctaggagg ctcgccgccc gcgcccgctc gttcggcctt   300

gcccgggacc gcgtcctgcc ccgagaccgc caccatgaac aagctttaca tcggcaacct   360

caacgagagc gtgacccccg cggacttgga gaaagtgttt gcggagcaca agatctccta   420

cagcggccag ttcttggtca aatccggcta cgccttcgtg gactgcccgg acgagcactg   480

ggcgatgaag gccatcgaaa ctttctccgg gaaagtagaa ttacaaggaa aacgcttaga   540

gattgaacat tcggtgccca aaaaacaaag gagccggaaa attcaaatcc gaaatattcc   600

accccagctc cgatgggaag tactggacag cctgctggct cagtatggta cagtagagaa   660

ctgtgagcaa gtgaacaccg agagtgagac ggcagtggtg aatgtcacct attccaaccg   720

ggagcagacc aggcaagcca tcatgaagct gaatggccac cagttggaga accatgccct   780

gaaggtctcc tacatccccg atgagcagat agcacaggga cctgagaatg ggcgccgagg   840

gggctttggc tctcggggtc agccccgcca gggctcacct gtggcagcgg gggccccagc   900

caagcagcag caagtggaca tcccccttcg gctcctggtg cccacccagt atgtgggtgc   960

cattattggc aaggaggggg ccaccatccg caacatcaca aaacagaccc agtccaagat   1020

agacgtgcat aggaaggaga acgcaggtgc agctgaaaaa gccatcagtg tgcactccac   1080

ccctgagggc tgctcctccg cttgtaagat gatcttggag attatgcata aagaggctaa   1140

ggacaccaaa acggctgacg aggttccccт gaagatcctg gcccataata actttgtagg   1200

gcgtctcatt ggcaaggaag gacggaacct gaagaaggta gagcaagata ccgagacaaa   1260

aatcaccatc tcctcgttgc aagaccttac cctttacaac cctgagagga ccatcactgt   1320

gaaggggggcc atcgagaatt gttgcagggc cgagcaggaa ataatgaaga agttcgggga   1380

ggcctatgag aatgatgtgg ctgccatgag cctgcagtct cacctgatcc ctggcctgaa   1440

cctggctgct gtaggtcttt cccagcttc atccagcgca gtcccgccgc ctcccagcag   1500

cgttactggg gctgctccct atagctcctt tatgcaggct cccgagcagg agatggtgca   1560

ggtgtttatc cccgcccagg cagtgggcgc catcatcggc aagaaggggc agcacatcaa   1620

acagctctcc cggtttgcca gcgcctccat caagattgca ccacccgaaa cacctgactc   1680

caaagttcgt atggttatca tcactggacc gccagaggcc caattcaagg ctcagggaag   1740

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gaccacata cgtgtgccag catcagcagc tggccgggtc attggcaaag gtggaaaaac   1860

ggtgaacgag ttgcagaatt tgacggcagc tgaggtggta gtaccaagag accagacccc   1920

tgatgagaac gaccaggtca tcgtgaaaat catcggacat ttctatgcca gtcagatggc   1980

tcaacggaag atccgagaca tcctggccca ggttaagcag cagcatcaga agggacagag   2040

taaccaggcc caggcacgga ggaagtgacc agccctccc tgtcccttcg agtccaggac   2100

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aacaacgggc agaaatcgag agtgtgctct ccccggcagg cctgagaatg agtgggaatc      2160

cgggacacct gggccgggct gtagatcagg tttgcccact tgattgagaa agatgttcca      2220

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cctcgggggtg tcagaaattc tagcgcaagg cacttttaaa cgtggattgt ttaaagaagc      2340

tctccaggcc ccaccaagag ggtggatcac acctcagtgg gaagaaaaat aaaatttcct      2400

tcaggtttta aaaacatgca gagaggtgtt ttaatcagcc ttaaaggatg gttcatttct      2460

tgaccttaat gttttttccaa tcttcttccc cctacttggg taattgatta aaatacctcc      2520

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atgcgaacga atgcattgct ttgcttacag tattgactca agggaaaaga actgtcagta      2640

tctgtagatt aattccaatc actccctaac caataggtac aatacggaat gaagaagagg      2700

ggaaaatggg gagaaagatg gttaaaatac ataataatcc acgtttaaaa ggagcgcact      2760

tgtggctgat ctatgccaga tcaccatctt caaattggca caactgaaat ttccccactc      2820

tgttggggct tccccaccac attcatgtcc ctctcccgtg taggtttcac attatgtcca      2880

ggtgcacata ggtggtattg aatgctcagc agggtagggg ctgaccactg tccctgattc      2940

ccatcgttct caggcggatt ttatattttt ttaaagtcta ttttaatgat tggatatgag      3000

cactgggaag gggacgctaa ctcccccttga taaagtctcg gttccatgga ggacttgagt      3060

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tcccatggag tgtttagccc ttgtgggaga cagaagccat cagttaaatg aggttaggcc      3480

tctcctccta atatactgat tgacaatgca tattagccag gtaatgcact ttagctaccc      3540

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tggtgggaaa ggctttgggg gctgccccct taggaggagg ctagtgctaa gagggaaggc      4020

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aattaagcct ctccacctgt cccaaccata aaaaggtct cccagctttc catctctggc     4860

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acccctttgg cctccagctt gtccctctct cactttctat agctttgttg gaccagatgg        7260

tgaggaaagg aatggcctct tcccttctag aggggctgg ctggagtgag acctggggct         7320

tggcctggaa cccaccacac agccccaaag tcaggaagcc tggggaaacc agagctgaga        7380

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tgggcgatcc cagcccctcc ccacccaccc tctaatggac ctcctcatag aagccccatt        7620

tcacttttgt tttatctacc tcttagcaaa acaatagata aattaggtag tggcagctcc        7680

acttgcttag gttaggggggg gaaaaagatt tcttttttcca aaggaaaaaa atattacctt       7740

gagaatactt tccaaaaaat aaaattaaaa aaaaaaaaac caaaaaaaaa aattttttttt        7800

taaaagggag acattttcca gtgaccactg gattgtttta atttcccaag cttttttttttc      7860

ccccataaat aagtttcact ctttggcgat tttcttcact tgtttaagat aacgtgctag        7920

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gaatttcagc agattatgtg ttaccataat gaataaacgt cctctatcac catttggagt        8280

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cctcccctga ggcaaagtgg atttgtaagc agttctgaaa catcacttac tcagaagagg        8400

gaacgatgta ttttgatgag tgcaaattgg gaagagctgg aggcctactg cttgggacag        8460

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<210> SEQ ID NO 588
<211> LENGTH: 577
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 588

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Asp Leu Glu Lys Val Phe Ala Glu His Lys Ile Ser Tyr Ser Gly Gln
            20                  25                  30
```

```
Phe Leu Val Lys Ser Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu His
        35              40              45

Trp Ala Met Lys Ala Ile Glu Thr Phe Ser Gly Lys Val Glu Leu Gln
        50              55              60

Gly Lys Arg Leu Glu Ile Glu His Ser Val Pro Lys Lys Gln Arg Ser
65              70              75              80

Arg Lys Ile Gln Ile Arg Asn Ile Pro Pro Gln Leu Arg Trp Glu Val
                85              90              95

Leu Asp Ser Leu Leu Ala Gln Tyr Gly Thr Val Glu Asn Cys Glu Gln
                100             105             110

Val Asn Thr Glu Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Asn
                115             120             125

Arg Glu Gln Thr Arg Gln Ala Ile Met Lys Leu Asn Gly His Gln Leu
        130             135             140

Glu Asn His Ala Leu Lys Val Ser Tyr Ile Pro Asp Glu Gln Ile Ala
145             150             155             160

Gln Gly Pro Glu Asn Gly Arg Arg Gly Gly Phe Gly Ser Arg Gly Gln
                165             170             175

Pro Arg Gln Gly Ser Pro Val Ala Ala Gly Ala Pro Ala Lys Gln Gln
                180             185             190

Gln Val Asp Ile Pro Leu Arg Leu Leu Val Pro Thr Gln Tyr Val Gly
                195             200             205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
        210             215             220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
225             230             235             240

Glu Lys Ala Ile Ser Val His Ser Thr Pro Glu Gly Cys Ser Ser Ala
                245             250             255

Cys Lys Met Ile Leu Glu Ile Met His Lys Glu Ala Lys Asp Thr Lys
                260             265             270

Thr Ala Asp Glu Val Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
        275             280             285

Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Val Glu Gln
        290             295             300

Asp Thr Glu Thr Lys Ile Thr Ile Ser Ser Leu Gln Asp Leu Thr Leu
305             310             315             320

Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Ala Ile Glu Asn Cys
                325             330             335

Cys Arg Ala Glu Gln Glu Ile Met Lys Lys Val Arg Glu Ala Tyr Glu
                340             345             350

Asn Asp Val Ala Ala Met Ser Leu Gln Ser His Leu Ile Pro Gly Leu
                355             360             365

Asn Leu Ala Ala Val Gly Leu Phe Pro Ala Ser Ser Ser Ala Val Pro
        370             375             380

Pro Pro Pro Ser Ser Val Thr Gly Ala Ala Pro Tyr Ser Ser Phe Met
385             390             395             400

Gln Ala Pro Glu Gln Glu Met Val Gln Val Phe Ile Pro Ala Gln Ala
                405             410             415

Val Gly Ala Ile Ile Gly Lys Lys Gly Gln His Ile Lys Gln Leu Ser
                420             425             430

Arg Phe Ala Ser Ala Ser Ile Lys Ile Ala Pro Pro Glu Thr Pro Asp
        435             440             445
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Ser Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
    450             455             460

Lys Ala Gln Gly Arg Ile Tyr Gly Lys Leu Lys Glu Glu Asn Phe Phe
465             470             475             480

Gly Pro Lys Glu Glu Val Lys Leu Glu Thr His Ile Arg Val Pro Ala
            485             490             495

Ser Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
            500             505             510

Leu Gln Asn Leu Thr Ala Ala Glu Val Val Val Pro Arg Asp Gln Thr
        515             520             525

Pro Asp Glu Asn Asp Gln Val Ile Val Lys Ile Ile Gly His Phe Tyr
    530             535             540

Ala Ser Gln Met Ala Gln Arg Lys Ile Arg Asp Ile Leu Ala Gln Val
545             550             555             560

Lys Gln Gln His Gln Lys Gly Gln Ser Asn Gln Ala Gln Ala Arg Arg
            565             570             575

Lys
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<210> SEQ ID NO 589
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 589

atttctatgc cagtcagatg g   21

<210> SEQ ID NO 590
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 590

gtgggcaaac ctgatctaca g   21

<210> SEQ ID NO 591
<211> LENGTH: 5016
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 591

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ggaggaaatg ttgtttttaa gggaaatgaa tagaaacaat ccactttgaa gaagccatgg   120

cgaaatcaaa gacaaaacat agactttgtt ctcaggaatc ttcagtatct gccctgctgg   180

caagctgcac cctgagtggt agtaattcct ctaattctga tggctcgttt cactataaag   240

ataagctgta cagatctgct tctcaagctc tacaggctta tattgatgat tttgatctag   300

gccaaatata tcctggtgca agcactggaa aaattaacat tgatgaggat tttactaata   360

tgtcacagtt ctgcaactat atttacaaac caaacaatgc ttttgaaaac cttgatcacg   420

aaaagcactc aaacttcata tcctgtagaa gacacatcgt taatgacata gactccatga   480

gcctaacaac tgatgatcta ttaagactcc cagcagatgg atcattttct tatacttatg   540

ttggaccgag tcaccgaacg agcaagaaaa acaagaaatg ccgtggaagg ctgggttcat   600
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tggacattga gaagaatcca cattttcaag gaccctacac ttccatgggc aaggataact    660

ttgttactcc tgttatacgc tcaaatataa atggaaagca atgtggtgac aaaattgaat    720

tgcttatctt gaaggccaag agaaatctag agcagtgtac tgaagaatta ccaaagtcca    780

tgaaaaagga tgacagtcct tgctcattag ataaacttga agcagacaga tcatgggaaa    840

atattcctgt tactttcaaa tctcctgttc ccgttaactc tgatgatagt cctcaacaaa    900

cttcaagggc aaagagtgct aaaggggttc ttgaagactt tctaaataat gataatcaga    960

gctgtactct ctctggaggc aaacatcatg gtcctgttga agccctgaaa caaatgttat   1020

ttaaccttca agcagtacaa gaacgtttta atcaaaataa gaccacagat ccaaaagaag   1080

agattaaaca gtttcagaa gatgatttct ctaaattaca gttgaaggaa agtatgattc    1140

ctattactag gtcacttcag aaggctttgc accatttatc tcgcctgaga gacctggttg   1200

atgatacgaa tggagaacgg tcaccgaaaa tgtgaagagg aaaatgaaac tgtcaccacg   1260

ataaatagtc accacagaac aaataggcat tttttctatt acttaaactg acaaagtaaa   1320

tataagccat acattatttt gtggttggtt caaggattat atatttctaa aacactaaac   1380

ttgaaaatac ccataggttt tgggacctat ctttattttg tgccaacata ctagaatgtg   1440

aactgcaagg acccacaatg tatcctgaag tcttactttc gccttctggc cagcaaatgt   1500

ctaatattta aagatggatg acttctgttc ttgaagctta cctggattta accttcttca   1560

gcatcctcaa cattttatta cctggttcag gatcattaag aaacttactg gttttttatcc  1620

aaaatctttt acgttaaata gacttttttta aagatatagt tagcatcact tttaaacagc   1680

ttaaaggaat atcaaaattg ttattgtgta tctcatctat aaggaagtct gttactttga   1740

aattttcata aatttaatat ttaagataca ttgtatttga aaattgcatt aatagtgggg   1800

tgatactgtg ttaaaaggaa cgttgtgttg tgacattcaa gagaacctcc tcatttaatt   1860

agtactttga ttctgtgtaa gataatcttg gtagtgcttg acagtttcca aacctttttt   1920

tggagagata tttaagaatt taatattttg atattagatt gtttcccaga ttttaatttt   1980

ggggttggct caaactagtg aaaactatga ctcaatggcc aattgcttta tcaaatttga   2040

taactaaaac ttaaaatgaa tatggaaaat cagaaagcaa ctctatttta gagctatttt   2100

gtaagagttg tgctttcttt aacaccatct gtagtcttaa gtttgtctct agctagaact   2160

gaacaaagct ctataatttt taccaagcac ttattattaa tacttcttat aagtagtaag   2220

catctttact aacacaactg agaattaagt cataaaacat aactaataca gcacattact   2280

gcctgacaaa attaaagagt actgtgtgta tgtataacta ctacaggtta acacttcacc   2340

caaatgatag cgttttttcct cagtagatta ttgtcaaata ggaatttcta agcacattga   2400

gtcaaagcat tttttccagg ttaataaagt gttatttact atctttgtta gaggtgacat   2460

gtcaaacact acagtgagct ctgtggggtt tttttttttt tttttgcccg tgagtttttt   2520

accatgctgc tctgaccagt ttgagtggca attaccaata gatttgtttt ctttattcta   2580

tggagatgtt tttaccactg acactgtttt ctgattatag tctgcttcat agaaaatagc   2640

ctgcataatc aaacaaggag ttactttgaa attaaagtat gcctggctat taaaaatgca   2700

gattttaggt gggtaaacat caggtaggtc tgggtgggtc atgttctagg cctagaaaaa   2760

tacactatta gacaagttct aaagaaggca aggagataaa ggcatcaggt ggtaacttct   2820

aattgaatat tatatgttga tcatacataa tatatactat gcctggaaat tatgactgaa   2880

aagcacctat tcggttagtg ctcctattca tgagaacata tctccaatac taaatgagat   2940
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aagcctgttc taaaatctta tagccagtat tttaagaaac ttgattatac ttaccaaagg      3000

aacattgttt gttttctctt gttttaaata tggagaggtt taatccttta cataacaaag      3060

gaattaattt tagcaaaatg attcattcca accttcttat aagaaatatc taggagagtc      3120

aagtaagaaa aataacgaat ctaagtgata aacattcaag aaattctcta aataagagat      3180

ttatttataa ttttaatatc tcagggttct ttttaggttt ccaggggaaa agagcaggat      3240

aacagtgtgg agactgctaa gttgagaatt taaaacaaat gagaacataa gatttttaaa      3300

attgcattgt gaatgtaaaa ttttatcaa tcctttgctc ttttagacat attgagaaaa       3360

tgttaaatag aaaaaattaa gaaattttaa taagatgttt cagatctttg agtatgaaaa     3420

acataacaaa aaagcctaat ttcaaaaaac tatttgagat caagggacaa tggtgtgacc      3480

aatatgaagg gtcaagactg aaatgtattg tctttactat caagaactct actttcagtt     3540

gtttctcaga cagttaattt cagcttcata gagatttctg agcaaattaa gaaacactgt      3600

tttcctgggt ttgttttggg tatatgtcat tatagttatg ttatttcttg ttgaaattta     3660

taattgtagg tttttttgtat tgttttggta tttaatggtg tataatgtgt tattacatta    3720

tatgtagtta taccaaaata ttgcctgaag agaaatcatg acaaggtccc ctgtttattc      3780

ctgtgttaca gacgcatgga attgctcctg tagatttgaa tttttgtttc attttttttct    3840

gtcccaccct tcactctctc tgtttcagaa catttttggt agaagtgcta tccagaagtg      3900

aacttgtcaa aaggcaagta gcatgaaaga agacagaaga agcaaaaggc taatacagtg      3960

gataatttct gagcacttga agtttcttca aatgtgcaag actgtgtgtc ttcctattag      4020

atgtataaat tggatatttc atgcctaatt aaatgttgcg ttggattgca gtgcctatca      4080

tacagtgatt ggagtaaatt gaggcctaat cctgaacaca tatagagcat attgttagat      4140

attttttcctg tgacatttga agttattatt ctcccatttc cttttctctt ttttgtttat    4200

aatcatatgt ccctaagatt gttttccttt tttggaccaa aaaaaagaaa aaaaaaatct      4260

tagcttttca tcctcccagt gtattctgca ttgtccttac cctagatcag cccccttctgt    4320

gtaacagttt ttctcacaat gtagcaactt ttatccaccc ttcaggacct tcactgggac      4380

tagttcattc attttcaaat agctatttca acctttaaca tctactgtct tagtctttta     4440

cacagaagcc agagtgactg gtcttggcaa gactctgttg tgtatcacca ctctaacctt      4500

actgatttgt ttcagcaaat ttgctttagt taaattgctt tactcagatt cccccaaact      4560

ttatatgtgt attgtcatct ttgtgcatat tatttctcat gcatgaaata ctcaattttt     4620

attcttttat ctaacgctta ctcttacatt tctttaaagc tctggccaag tattttattt     4680

cgtccctaaa cattctaact atccaccaaa ctggtaagtt ggcttttctt tttcctcccc      4740

ctgtcattca tttagctgtt atatttcatt ttaatgtttt gggtggtgcc tcttatacta     4800

tgttgtattc ctagacaagg aaatgtatat caaaatatgt tagatgattg attgtttttat    4860

ctccttgatg atagcacctc ttatactgct ttacagaatc aggaaaaagt aaactgcatt     4920

ttacatagtg gttttaaata ttgattgatt gatattctaa acctggtttc ctatataaag     4980

ttgtaagttc aagataaaaa aaaaaaaaaa aaaaca                                5016
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<210> SEQ ID NO 592
<211> LENGTH: 372
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 592

Met Ala Lys Ser Lys Thr Lys His Arg Leu Cys Ser Gln Glu Ser Ser

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1                5                    10                   15
Val Ser Ala Leu Leu Ala Ser Cys Thr Leu Ser Gly Ser Asn Ser Ser
             20              25              30

Asn Ser Asp Gly Ser Phe His Tyr Lys Asp Lys Leu Tyr Arg Ser Ala
             35              40              45

Ser Gln Ala Leu Gln Ala Tyr Ile Asp Asp Phe Asp Leu Gly Gln Ile
       50              55              60

Tyr Pro Gly Ala Ser Thr Gly Lys Ile Asn Ile Asp Glu Asp Phe Thr
65              70              75              80

Asn Met Ser Gln Phe Cys Asn Tyr Ile Tyr Lys Pro Asn Asn Ala Phe
                 85              90              95

Glu Asn Leu Asp His Glu Lys His Ser Asn Phe Ile Ser Cys Arg Arg
             100             105             110

His Ile Val Asn Asp Ile Asp Ser Met Ser Leu Thr Thr Asp Asp Leu
             115             120             125

Leu Arg Leu Pro Ala Asp Gly Ser Phe Ser Tyr Thr Tyr Val Gly Pro
       130             135             140

Ser His Arg Thr Ser Lys Lys Asn Lys Lys Cys Arg Gly Arg Leu Gly
145             150             155             160

Ser Leu Asp Ile Glu Lys Asn Pro His Phe Gln Gly Pro Tyr Thr Ser
                 165             170             175

Met Gly Lys Asp Asn Phe Val Thr Pro Val Ile Arg Ser Asn Ile Asn
             180             185             190

Gly Lys Gln Cys Gly Asp Lys Ile Glu Leu Leu Ile Leu Lys Ala Lys
             195             200             205

Arg Asn Leu Glu Gln Cys Thr Glu Glu Leu Pro Lys Ser Met Lys Lys
       210             215             220

Asp Asp Ser Pro Cys Ser Leu Asp Lys Leu Glu Ala Asp Arg Ser Trp
225             230             235             240

Glu Asn Ile Pro Val Thr Phe Lys Ser Pro Val Pro Val Asn Ser Asp
                 245             250             255

Asp Ser Pro Gln Gln Thr Ser Arg Ala Lys Ser Ala Lys Gly Val Leu
             260             265             270

Glu Asp Phe Leu Asn Asn Asp Asn Gln Ser Cys Thr Leu Ser Gly Gly
             275             280             285

Lys His His Gly Pro Val Glu Ala Leu Lys Gln Met Leu Phe Asn Leu
       290             295             300

Gln Ala Val Gln Glu Arg Phe Asn Gln Asn Lys Thr Thr Asp Pro Lys
305             310             315             320

Glu Glu Ile Lys Gln Val Ser Glu Asp Asp Phe Ser Lys Leu Gln Leu
             325             330             335

Lys Glu Ser Met Ile Pro Ile Thr Arg Ser Leu Gln Lys Ala Leu His
             340             345             350

His Leu Ser Arg Leu Arg Asp Leu Val Asp Asp Thr Asn Gly Glu Arg
             355             360             365

Ser Pro Lys Met
       370
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<210> SEQ ID NO 593
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide
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<400> SEQUENCE: 593

aatggaaagc aatgtggtga c   21

<210> SEQ ID NO 594
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 594

tccagagaga gtacagctct g   21

<210> SEQ ID NO 595
<211> LENGTH: 2061
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 595

atgaggcgga caggccccga ggaggaggcc tgcggcgtgt ggctggacgc ggcggcgctg   60

aagaggcgga aagtgcagac acatttaatc aaaccaggca ccaaaatgct aacactcctt   120

cctggagaaa gaaaggctaa tatttatttt actcaaagaa gagctccatc tacaggcatt   180

caccagagaa gcattgcttc cttcttcacc ttgcagccag aaagacaaa tggcagtgac   240

cagaagagtg tttcatctca tacagaaagt cagatcaaca agagtccaa gaaaaatgcg   300

acccagctag accatttgat cccaggctta gcacacgatt gcatggcatc ccctttagcc   360

acttcaacca ctgcggacat ccaggaagct ggactctctc ctcagtccct ccagacttct   420

ggccaccaca gaatgaaaac cccatttttca actgagctat ctttgctcca gcctgatact   480

ccagactgtg ctggagatag tcatacccca ctggctttt ccttcaccga ggacttggaa   540

agttcttgtt tgctagaccg aaaggaagaa aaagggggatt ctgccaggaa atgggaatgg   600

cttcatgagt ctaagaagaa ctatcagagt atggagaaac acaccaaact acctggggac   660

aaatgctgtc agcccttagg caagactaaa ttggaaagaa aggtgtctgc caaagaaaac   720

aggcaggccc ctgtcctcct tcaaacatac agggaatcct ggaatggaga aaacatagaa   780

tcggtgaaac aaagccgtag tccagtttct gtgttttcct gggacaatga aaagaatgac   840

aaggactcct ggagtcaact tttcactgaa gattctcaag ccagcgggt cattgcccac   900

aacactagag ctcctttttca agatgtaacc aataactgga attgggactt agggccgttt   960

cctaacagtc cttgggctca gtgccaggag gatgggccaa ctcaaaatct gaagcctgat   1020

ttgctcttta cccaggactc tgaaggtaat caagttatca gacaccaatt ctaaatgttt   1080

gaagctttgt ttctaaaagt accttgaaat gatagagatg taggaaaata tagttgtggg   1140

tggagagagg agtgagtttg tttaggtggg aaggtggcat gggatgaagt tgtcattact   1200

gagcatcttc tctgtgtaaa taaagggcag taccattgtt aagacagtgg gattggcatc   1260

atggctttcc ctcaggaagg tggtggctgg taaattccct gaatgagtct atgatgaaca   1320

ctgaggcagc acagtgggta tttatctcta tgaaagtgcc ttttactcag cctgcacaga   1380

gccatctctt tgcccttcca gatgtctgac tgggaccttg cttatggatg tgtttttttt   1440

tttttttttt tgagatggag tctcgctctg tcgccaggct ggagtgcagt ggtgcgacct   1500

cagctcactg caccctctgt gtcccggatt caagcgattc tcctgcctca gcctcccgaa   1560

tagcagggac tacaggcatg cgccaccacg cccagctaat ttttttttgga tttttagtag   1620

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agacgaggtt tcaccatatt agccaggatg gtctccatct cctgacctcc tgatccgccc    1680

acctcagcct cccaaagtgc tgagattaca ggcataagcc accgcgccca gccagatgtg    1740

tgagctttta atctctggct gatcttaacc cacatcagcc taagcttggg atgattactc    1800

ttgacccttt tttttcagtg attagcaaat ctccccacaa cccaggtgtg gagagaagag    1860

aggtagaatg gtgctagttt cctattttat ttttgtggta actgtacagc actttaaagt    1920

tatatactct atgtttaaat atctccctta aaaagcctga gctgtacaac aatctggatg    1980

tgactctgtt acccttttcc cacaagatag gagggaatcc cctttgtaaa actatgaatc    2040

caaataaatg tttacaaagt g    2061
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<210> SEQ ID NO 596
<211> LENGTH: 357
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 596

Met Arg Arg Thr Gly Pro Glu Glu Glu Ala Cys Gly Val Trp Leu Asp
1               5                   10                  15

Ala Ala Ala Leu Lys Arg Arg Lys Val Gln Thr His Leu Ile Lys Pro
            20                  25                  30

Gly Thr Lys Met Leu Thr Leu Leu Pro Gly Glu Arg Lys Ala Asn Ile
        35                  40                  45

Tyr Phe Thr Gln Arg Arg Ala Pro Ser Thr Gly Ile His Gln Arg Ser
    50                  55                  60

Ile Ala Ser Phe Phe Thr Leu Gln Pro Gly Lys Thr Asn Gly Ser Asp
65                  70                  75                  80

Gln Lys Ser Val Ser Ser His Thr Glu Ser Gln Ile Asn Lys Glu Ser
                85                  90                  95

Lys Lys Asn Ala Thr Gln Leu Asp His Leu Ile Pro Gly Leu Ala His
            100                 105                 110

Asp Cys Met Ala Ser Pro Leu Ala Thr Ser Thr Thr Ala Asp Ile Gln
        115                 120                 125

Glu Ala Gly Leu Ser Pro Gln Ser Leu Gln Thr Ser Gly His His Arg
    130                 135                 140

Met Lys Thr Pro Phe Ser Thr Glu Leu Ser Leu Leu Gln Pro Asp Thr
145                 150                 155                 160

Pro Asp Cys Ala Gly Asp Ser His Thr Pro Leu Ala Phe Ser Phe Thr
                165                 170                 175

Glu Asp Leu Glu Ser Ser Cys Leu Leu Asp Arg Lys Glu Glu Lys Gly
            180                 185                 190

Asp Ser Ala Arg Lys Trp Glu Trp Leu His Glu Ser Lys Lys Asn Tyr
        195                 200                 205

Gln Ser Met Glu Lys His Thr Lys Leu Pro Gly Asp Lys Cys Cys Gln
    210                 215                 220

Pro Leu Gly Lys Thr Lys Leu Glu Arg Lys Val Ser Ala Lys Glu Asn
225                 230                 235                 240

Arg Gln Ala Pro Val Leu Leu Gln Thr Tyr Arg Glu Ser Trp Asn Gly
                245                 250                 255

Glu Asn Ile Glu Ser Val Lys Gln Ser Arg Ser Pro Val Ser Val Phe
            260                 265                 270

Ser Trp Asp Asn Glu Lys Asn Asp Lys Asp Ser Trp Ser Gln Leu Phe
        275                 280                 285
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Thr Glu Asp Ser Gln Gly Gln Arg Val Ile Ala His Asn Thr Arg Ala
    290                 295                 300

Pro Phe Gln Asp Val Thr Asn Asn Trp Asn Trp Asp Leu Gly Pro Phe
305                 310                 315                 320

Pro Asn Ser Pro Trp Ala Gln Cys Gln Glu Asp Gly Pro Thr Gln Asn
                325                 330                 335

Leu Lys Pro Asp Leu Leu Phe Thr Gln Asp Ser Glu Gly Asn Gln Val
            340                 345                 350

Ile Arg His Gln Phe
        355


<210> SEQ ID NO 597
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 597

caccttgcag ccaggaaaga c                                                    21


<210> SEQ ID NO 598
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 598

cagcacagtc tggagtatca g                                                    21


<210> SEQ ID NO 599
<211> LENGTH: 1907
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 599

aatgcacacg agcagacaga gaagcaacat ctttaaggta ctgagggcag gagaagttaa       60

tgtagaatac tatgccagaa aaaataaatt cccaaaagtg gaagtgaaat aaggacattt      120

agagatgtac aaaagctgac cgaattcact accagtcaac ccacactaca agaaacatca      180

aatgagtcct ccaagcagaa ggaatccaat accagatgaa aatccagatc tccacgagga      240

aatgaagaac accagaaatg ggtaactata ctagatcggc cctttcttca aataagagca      300

gttggaataa caaagctgtt cagttgtacc cttggaatcc actgaaatcc tgggtaggga      360

agctccagta ccaccaactg gaaagactgg gaatgcctaa tagctggtac tggccattgt      420

cgtaggcttt gtccactctg acaaactgaa gatggggact cgactcacct tcgccagcca      480

caggaggacc tccagacgag gacaggactc gctgcctttc tttcccgtca gaaagggatc      540

ccttgcggac aggacctaag caccacgcac ctgcccccg ggatgccgaa cgaagtggtc      600

cctaaagctc ctctgcaggc ccaaccgaaa caggcctgaa gctccaggat gggcgagagg      660

atcctctttg agcgaaacca gccttctgcc tggctggccc tggtcaacac cctgggaaga      720

ggccgatttg gcggacagaa cggaagaaaa gacctaaagg tagaatctca tgatgtcgag      780

atgttaaaac actcaaattt taaggttcga ctgtgagggg gagataggg gtctcgagct      840

ggatcgaccc ctgagccttc atctgcagag tcctgtgcac cagctcagag gacaggacta      900
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tgtgcaccaa tggttctcat caggcggcaa cttcaccctc acatgcctcc cccatccctg      960

ctggtacaca agaccacgac taggggaagc ccggagggag aatgttaacc cctggcatct     1020

atctagtcag cagaggtgag ggatgctgct aaacaccta caatccaccg gaggacaccc     1080

gcccccaccg accccgaagt ggccattccc tggaggtggg gaaactcgcc tgtagatcaa     1140

tgcccacgca cttggcggac aggaaatcac gaattggcca ctaactggat cttggatctg     1200

agaaaaaaat tccagcgtca gagggaactc tcggagattt gcccagagca taaggaacgt     1260

actccttccc tcagtgatgg atcctcacat ctggggaaa tcatagacaa tttcttttgt     1320

agggcgaact ctgctataca gtttatgatg tcagagtgaa tactttcttt gagttgcagt     1380

cagaaactgt agatttttaa aaatttaaaa ttcattattc tctgtcagta ttccaaagtg     1440

tatacagaaa gctattgcac tgttcaggag atggcgctta acattttgga aattcaaggt     1500

gatgaatgtc cagataagac tatctctcct ggtacaaagt ttgacaatgc tgaacatttt     1560

taaaggttct ttttgatata caaagtgcac caatgagtgc tttttaattc ttacaataat     1620

tctgggtgag gtaggtattt ttccaattcc cattttatgc ttcggtagcc ctttgtattt     1680

atacttcaaa acacttggct ctcttgtaat tatttaagaa attagttgtg attatttgtt     1740

taatgtgcag gagttacaaa aggcaagctt tagaacaaga cagacctggt tatgattcct     1800

ggctctgaaa gctgtacacc ctgtgaccct agacaggtgt tttaatgcct cgctgcctct     1860

gtttcttgct ctgtaaaatg tgaacaataa cagtattggc ctcatgc                  1907
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<210> SEQ ID NO 600
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 600

ttgcggacag gacctaagca c                                                  21


<210> SEQ ID NO 601
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 601

tagtcctgtc ctctgagctg g                                                  21


<210> SEQ ID NO 602
<211> LENGTH: 2553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 602

tgcgtgtcgg ggtccgctcg tgcgcgcctc tccggggtct gtgcgcgtgg ccctccgctc      60

gcgccggagg gcgtgggcgt ggcctcggcg tgggtgtggc cgctcgggga ggggcctccc     120

gggggcgggg ccggcctggt ccgcgcggtg acgcgccctg cagccccgag cgagcgagcg     180

agcgagcgag ttgccgagcg cgccccgtcc ctcgcgcgcg atgctccct ggacggcgct     240

cggcctggcc ctgagcttgc ggctggcgct ggcgcggagc ggcgcggagc gcggtccacc     300

agcatcagcc ccccgagggg acctgatgtt cctgctggac agctcagcca gcgtctctca     360
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ctacgagttc tcccgggttc gggagtttgt ggggcagctg gtggctccac tgccctgggg    420

caccggggcc ctgcgtgcca gtctggtgca cgtgggcagt cggccataca ccgagttccc    480

cttcggccag cacagctcgg gtgaggctgc ccaggatgcg gtgcgtgctt ctgcccagcg    540

catgggtgac acccacactg gcctggcgct ggtctatgcc aaggaacagc tgtttgctga    600

agcatcaggt gcccggccag gggtgcccaa agtgctggtg tgggtgacag atggcggctc    660

cagcgaccct gtgggccccc ccatgcagga gctcaaggac ctgggcgtca ccgtgttcat    720

tgtcagcacc ggccgaggca acttcctgga gctgtcagcc gctgcctcag ccctgccga    780

gaagcacctg cactttgtgg acgtggatga cctcacatc attgtccaag agctgagggg    840

ctccattctc gacgcgatgc ggccgcagca gctccatgcc acggagatca cgtccagcgg    900

cttccgcctg cctggccac ccctgctgac cgcagactcg ggctactatg tgctggagct    960

ggtgcccagc gcccagccgg gggctgcaag acgccagcag ctgccaggga cgccacgga    1020

ctggatctgg gccggcctcg acccggcac ggactacgac gtggcgctag tgcctgagtc    1080

caacgtgcgc ctcctgaggc cccagatcct gcgggtgcgc acgcggcccg gtgaggcagg    1140

gccggggct tcgggcccgg agtcgggggc tgggccggcc cccacgcagc tcgccgccct    1200

ccccgcccca gaggaggccg ggccagagcg catcgtcatc tcccacgccc ggccgcgcag    1260

cctccgcgtg agttgggccc cagcgctggg ctcagccgcg gcgctcggct accacgtgca    1320

gttcgggccg ctgcggggcg gggaggcgca gcgggtggag gtgcccgcgg ccgcaactg    1380

caccacgctg cagggcctgg cgccggggcac cgcctacctg gtgaccgtga ccgccgcctt    1440

ccgctcgggc cgcgagagcg cgctgtccgc caaggcctgc acgcccgacg gcccgcgccc    1500

gcgcccacgc cccgtgcccc gcgccccgac cccggggacc gccagccgtg agccgtaagc    1560

cggcgtcccc gcccagccga gagggccggc gcctacctga gggcccctgt gtcccgaacc    1620

cggagcggag gcgcccaacc cggcagacg gtgcaggccc ggcctttccc cacgcggact    1680

ccgcgcgacc ccggccctct ccctgcggcc gcagggcttc cccgcctggc gcctgccctc    1740

cagggctggg gcctcgcctg gcgggacccc gcagcagccc cggcccatc cccgcccaga    1800

gccgggcgtc gtgtgggtcc gtgggtgata attgagagcg tcagacccag gactgttcag    1860

ggaggagccc cggtcagact cccacgtgtg aagaccgggc cccaagtggc aagggctggc    1920

ctggggcggg cagcttgggt cctggacgtt gataggaagc ggaaggggaa tcgcgggaag    1980

ctggcccagg tcaggtccgc aaaggcttct gaagaagagg aagggcgagt aggggcacct    2040

ggacgctgat ggtggccagg atgctcagct ggccaggagg gcagcacctg ctggggacgg    2100

tggccctgcc ttcatgccca ggacaccagc tgggtccagc tagcagccac tgggaatcag    2160

aggaatgggg cagagctggg cattcaggac cttgaggaca cgtgacccca cccgcccacc    2220

gccactatca ggccccggga ccgcactgac aggaaacctt ccgtcgtgag ggagcacttc    2280

ccaggggccg cagggacgac actctccagg gaggccccag caaccacacc atcttcttgc    2340

tgtgagaggt ctcaccccgg gctacctcct gtcactactc actgccctgg ggtccgtggg    2400

caagttgccc agggtggggg tgcctagcca ggtgcagtcc ccgccccgcc tagtcctcgg    2460

cgtcacgcaa tgctcacctc gcctcttccc cactaacatc ccagacttta aaattcagta    2520

aatcagatgt acaccgaaaa aaaaaaaaaa aaa    2553
```

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<210> SEQ ID NO 603
<211> LENGTH: 445
<212> TYPE: PRT
```

```
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 603

Met Leu Pro Trp Thr Ala Leu Gly Leu Ala Leu Ser Leu Arg Leu Ala
1               5                   10                  15

Leu Ala Arg Ser Gly Ala Glu Arg Gly Pro Pro Ala Ser Ala Pro Arg
            20                  25                  30

Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr
        35                  40                  45

Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu
    50                  55                  60

Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
65                  70                  75                  80

Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala
                85                  90                  95

Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His
            100                 105                 110

Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala
        115                 120                 125

Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
    130                 135                 140

Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
145                 150                 155                 160

Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu
                165                 170                 175

Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe
            180                 185                 190

Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser
        195                 200                 205

Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr
    210                 215                 220

Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser
225                 230                 235                 240

Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala
                245                 250                 255

Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile Trp Ala Gly
            260                 265                 270

Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro Glu Ser Asn
        275                 280                 285

Val Arg Leu Leu Arg Pro Gln Ile Leu Arg Val Arg Thr Arg Pro Gly
    290                 295                 300

Glu Ala Gly Pro Gly Ala Ser Gly Pro Glu Ser Gly Ala Gly Pro Ala
305                 310                 315                 320

Pro Thr Gln Leu Ala Ala Leu Pro Ala Pro Glu Glu Ala Gly Pro Glu
                325                 330                 335

Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser Leu Arg Val Ser Trp
            340                 345                 350

Ala Pro Ala Leu Gly Ser Ala Ala Ala Leu Gly Tyr His Val Gln Phe
        355                 360                 365

Gly Pro Leu Arg Gly Gly Glu Ala Gln Arg Val Glu Val Pro Ala Gly
    370                 375                 380

Arg Asn Cys Thr Thr Leu Gln Gly Leu Ala Pro Gly Thr Ala Tyr Leu
385                 390                 395                 400
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Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg Glu Ser Ala Leu Ser
            405                 410                 415

Ala Lys Ala Cys Thr Pro Asp Gly Pro Arg Pro Arg Pro Arg Pro Val
            420                 425                 430

Pro Arg Ala Pro Thr Pro Gly Thr Ala Ser Arg Glu Pro
        435                 440                 445


<210> SEQ ID NO 604
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 604

aaccaacctg aggatttcac g                                              21


<210> SEQ ID NO 605
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 605

agacagctgt tcgtgagaag c                                              21


<210> SEQ ID NO 606
<211> LENGTH: 1999
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 606

cactctgtaa gttcaccgcc ggtcgggtcc ggccgccgcg ctgtccagct cctgagacct      60

tgctgtccgc cggtctgccg tctgcgcgcc tcacgctcct cagccctgga ccggggacaa     120

gtaaccctcg gtgacaagac caaagtgcac tgctgcccac acagttccta cctttctggc     180

ttcaattctt cagaagagtt tgccgtcctt tggggagaac gtgatttttg ttatctcagc     240

ccactgactt cattgatctc taatcttttt taattccttg ggccaacttt gttcgtgccc     300

ccacactgta gccagaagcc cgttggcgag ctctggcacc tgcaaaccac cccgtggaac     360

gagtgtttcc tctggctgag ggttggagag gaggtgtggt ctcagcaggc ggcccgtagc     420

ctcacagcca ggcctggtgg tgaggtcacc atgtccacca aggtgcccat ctatctgaag     480

cgtggcagtc gcaagggcaa gaaggagaag cttcgggacc tgctgtcctc ggacatgatc     540

agcccaccgc tggggactt ccgccacacc attcatattg gcagtggcgg cggcagtgac     600

atgtttggcg acatctcctt cctgcagggc aagttccacc tcctgccggg gaccatggtg     660

gagggggctg aagaagatgg caccttcgac ctccccttcc agttcacccg caccgccacc     720

gtgtgtgggc gggagctccc ggacggccca tccctctgc tcaagaacgc catctccctc     780

ccggttatcg gtggacccca ggctctcacc ctgcccacag cccaggctcc acccaagccc     840

cctcgcctgc acctggagac ccctcagcct tccccacagg agggagggag tgtggacatc     900

tggaggattc cagagactgg ctcccccaac agtggactga ccccggagtc aggggccgag     960

gagcccttcc tgtccaatgc cagctccctg ctgtccctgc acgtggacct ggggccttcc    1020

atcctggatg atgtcctgca gatcatggat caggacctgg acagcatgca gatccccaca    1080
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taggacacga ggctgcctag gctggggtcc caggtggggc ccagccagga ggtgggggtgt    1140

ggacccggcc ctggcggcgg agtcagggtc ccaagatccc acctgtatgg tcgctggcca    1200

gtgattctcc ttctgagccg tgtttcccct ctccctccct ctccacgtgg gcagggcagg    1260

ccccatcgct ttcctctgat aaccacatgg acacatcctg aagtcagccc aggcgccctg    1320

agcatcttgg ggcacctgga ccccatcaca atactccttc ttccttcagg tccctgggtg    1380

aaggctttgc tgaaaccgac cccccttttc acgtcccttc tgcctctgcc ccgttggatg    1440

ccctgactgg gggcagggga agagacaggg cacagctggc cacagggctc agccactgag    1500

caggctgttc cgggcctttg gctttgcatc ctggacgggg agtgtcctgt cagggaccag    1560

atgtgtcctg cctcatccct agctccaatc ccttccccac gtgaccgggg attctggttg    1620

caataaaaca tgctgctgct ggtggcggag ctccctgtcc cttTgcccca ggtttcctcc    1680

cggaggcaga cagtctccca gagctgaggg cttgcctctg gagaccccag ccccagaggg    1740

ctttgtggag gacaggcctt gccctcaaga acgtcgtacc tgacgctgag cctgtcatga    1800

gaatgcaaca ggagcaaacc aagtgttgct gtgacattga ttcagatgtt tggcaagagg    1860

tggctgagca ctgggtgggg cttggcactg tgccaagcct ggggccaatc cctgcccagt    1920

cagctggggt ctggtggggg acacccaaga ataaagaat aaccacaaag tgtgcaaggg    1980

aaaaaaaaaa aaaaaaaaa                                                  1999
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<210> SEQ ID NO 607
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 607

Met Ser Thr Lys Val Pro Ile Tyr Leu Lys Arg Gly Ser Arg Lys Gly
1               5                   10                  15

Lys Lys Glu Lys Leu Arg Asp Leu Leu Ser Ser Asp Met Ile Ser Pro
            20                  25                  30

Pro Leu Gly Asp Phe Arg His Thr Ile His Ile Gly Ser Gly Gly Gly
        35                  40                  45

Ser Asp Met Phe Gly Asp Ile Ser Phe Leu Gln Gly Lys Phe His Leu
    50                  55                  60

Leu Pro Gly Thr Met Val Glu Gly Pro Glu Glu Asp Gly Thr Phe Asp
65                  70                  75                  80

Leu Pro Phe Gln Phe Thr Arg Thr Ala Thr Val Cys Gly Arg Glu Leu
                85                  90                  95

Pro Asp Gly Pro Ser Pro Leu Leu Lys Asn Ala Ile Ser Leu Pro Val
            100                 105                 110

Ile Gly Gly Pro Gln Ala Leu Thr Leu Pro Thr Ala Gln Ala Pro Pro
        115                 120                 125

Lys Pro Pro Arg Leu His Leu Glu Thr Pro Gln Pro Ser Pro Gln Glu
    130                 135                 140

Gly Gly Ser Val Asp Ile Trp Arg Ile Pro Glu Thr Gly Ser Pro Asn
145                 150                 155                 160

Ser Gly Leu Thr Pro Glu Ser Gly Ala Glu Glu Pro Phe Leu Ser Asn
                165                 170                 175

Ala Ser Ser Leu Leu Ser Leu His Val Asp Leu Gly Pro Ser Ile Leu
            180                 185                 190

Asp Asp Val Leu Gln Ile Met Asp Gln Asp Leu Asp Ser Met Gln Ile
        195                 200                 205
```

Pro Thr
    210

<210> SEQ ID NO 608
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 608

aacgtcgtac ctgacgctga g   21

<210> SEQ ID NO 609
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 609

ccaagtgttg ctgtgacatt g   21

<210> SEQ ID NO 610
<211> LENGTH: 986
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 610

attcaagatg atgttagaga gatgacagag tctaggttag ggagggcctg agtccttgta   60

gactctgagt acggtgctga gcagggaaga gacaggctct ggcttagggt ttagaaggaa   120

cacaggctac tgcgatgagg attgtctgaa ggggaacaaa ggccaagatg ttgtttgaag   180

ccgtgagact gagtgagatc atggaggaag tgaatgtaaa tagaaaaggg aagaagtctg   240

aagacggagc cctgagacac tccattgtaa actggaagat gaggaagagc cagcaaagga   300

gactgagaag gggcagccag tgaagatgga gccagggcta gagtaagagc cccttctggg   360

atgctgtgac ccccaagttt gaagactgct gataacccca atctacgaag actagctatg   420

gaacttccta cactgagaca actccagtgg aactctgata attatcctaa aataaggagg   480

cttcttcagt agccctcgaa atatgttcaa atacatgatt acatttatgt ccttaatatt   540

gctattagtt tctgatgtta atgtaaaagt tggggaaaaa gtggaaaagt taaagcagtg   600

caggttaatt caatgccaga gtaacttctc agagggtgta tattcagtgt gaacaatttt   660

caacagagaa atgtcaactt ctggccacaa cggcaaccag taaaatgact atttttactg   720

tcttatctat taatgaagag gagattgcat aatatagatg aaggagcata gtatttgcag   780

gtggaacgcc tagcagggct tgagtctcaa ctctgctgct tttactctaa ttgaccgaga   840

caagtcattt aaactaatag agcttcaatt ttctcatatc taatgtaaca taacaattca   900

cagcctttta ctttgtagtt atcgtgaaga tctaatcgca gtgaaatata tttatatatc   960

tgtctgccga taaaaaaaaa aaaaaa   986

<210> SEQ ID NO 611
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 611

gactctgagt acggtgctga g   21

<210> SEQ ID NO 612
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 612

tcttactcta gccctggctc c   21

<210> SEQ ID NO 613
<211> LENGTH: 899
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 613

cccgagcgcc ggccgggcca tgaccccgc tgctctgtct tgcaggctcg tcgccgcggc   60

cccccgagcc cgaccgccgc cgccaccacc accagcgccc gggcgggcct cgcgcgcctc   120

gggcgcggct ccgcagtgag cccaccaaga aggaagcggc ctgcagaggt gccgacatgg   180

ggcttaagat gtcctgcctg aaaggctttc aaatgtgtgt cagcagcagc agcagcagcc   240

acgacgaggc ccccgtcctg aacgacaagc acctggacgt gcccgacatc atcatcacgc   300

cccccacccc cacgggcatg atgctgccga gggacttggg gagcacagtc tggctggatg   360

agacagggtc gtgcccagat gatggagaaa tcgacccaga agcctgagga ggtgtcctgg   420

gtttggctgg ctggctcctg ctccagcggc ccggcttcag gtgtccgggg gcgtggctgc   480

ctggagcagg tgtgctgaat accctggatg ggaactgagc gaacccgggc ctccgctcag   540

agagacgtgg caggaccagc gaggaatcca gcctgtccac ttccagaaca gtgtttccca   600

ggccccgctg agtggaccgg acctctgaca cctccaggtt cttgctgact ccggcctggt   660

gaaagggagc gccatggtcc tggctgttgg ggtcccaggg agaggctctc ttctggacaa   720

acacaccctc ccagcccca gggctgtgca aacacatgcc cctgccataa gcaccaacaa   780

gaacttcttg caggtggagt ggctgttttt tataagttgt tttacagata cggaaacagt   840

ccaaaatggg atttataatt tctttttttgc attataaata aagatcctct gtaacaaaa   899

<210> SEQ ID NO 614
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 614

Met Gly Leu Lys Met Ser Cys Leu Lys Gly Phe Gln Met Cys Val Ser
1   5   10   15

Ser Ser Ser Ser Ser His Asp Glu Ala Pro Val Leu Asn Asp Lys His
                20   25   30

Leu Asp Val Pro Asp Ile Ile Ile Thr Pro Pro Thr Pro Thr Gly Met
            35   40   45

Met Leu Pro Arg Asp Leu Gly Ser Thr Val Trp Leu Asp Glu Thr Gly
        50   55   60

Ser Cys Pro Asp Asp Gly Glu Ile Asp Pro Glu Ala
65   70   75

```
<210> SEQ ID NO 615
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 615

tgtcctgcct gaaaggcttt c                                            21


<210> SEQ ID NO 616
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 616

catccagggt attcagcaca c                                            21


<210> SEQ ID NO 617
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 617

ttatgtgcct gaagtcgcac agtgaataag ctaaaacacc tgcttttaac aatggtacca    60

tacaaccact actccattaa ctccacccac ctcctgcacc cctccccaca cacacaaaat   120

gaaccacgtt ctttgtatgg gcccaatgag ctgtcaagct gccctgtgtt catttcattt   180

ggaattgccc cctctggttc ctctgtatac tactgcttca tctctaaaga cagctcatcc   240

tcctccttca cccctgaatt tccagagcac ttcatctgct ccttcatcac aagtccagtt   300

ttctgccact agtctgaatt tcatgagaag atgccgattt ggttcctgtg ggtcctcagc   360

actattcagt acagtgcttg actcacagca ggcactcaga aaatactgga ggaaataaaa   420

caccaaagat at                                                      432


<210> SEQ ID NO 618
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 618

ctgctccttc atcacaagtc c                                            21


<210> SEQ ID NO 619
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 619

gagatctcga gatctcgatc gtac                                         24


<210> SEQ ID NO 620
<211> LENGTH: 2575
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 620

```
gagaacggg  tagcccggcg  cttacacatg  tcacatgtgc  tttttaagac  ggccgggagc    60

gcctgcgagc  tggatctggt  ggaggatgct  gcggcaggtg  cttcgcagag  ggctccagtc   120

gttctgccac  aggctgggtt  tgtgcgtgag  ccggcacccg  gtcttttttcc  tcaccgtgcc   180

cgcagtcctg  acaatcacct  tcggcctcag  cgcgctcaac  cgcttccagc  ccgagggcga   240

cctggagcgc  ctggtcgctc  ccagccacag  cctggccaag  atcgagcgca  gcctggccag   300

cagccttttc  cccctggacc  agtccaaaag  ccagctctat  tcggacttac  acacccctgg   360

gaggtatggc  agggtgatcc  tcctctcccc  aaccggggac  aatattttgc  tccaggctga   420

ggggatcctg  cagacccacc  gagccgtgct  ggaaatgaag  gatgggagga  acagttttat   480

tggacaccaa  ctgggcgggg  tagtggaagt  gccaaacagc  aaagatcagc  gggtcaagtc   540

agccagagcc  attcaaatca  cctactacct  ccagacctat  ggctctgcca  cccaagacct   600

cataggggag  aagtgggaga  atgagttctg  taagcttata  aggaagctcc  aggaggagca   660

tcaagaactc  cagctctact  ctttagcatc  ctttagcctc  tggagggact  ttcataagac   720

cagcatcctg  gccagaagca  aggtcctggt  gagcctcgtg  ctgatcctga  ccacagccac   780

cctctccagc  tccatgaagg  actgcttgcg  cagtaagccc  ttcctgggcc  tcctgggggt   840

gctcacagta  tgcatctcca  tcatcacagc  agcagggatc  ttcttcatca  ccgatggaaa   900

gtacaactcc  accctgctgg  gaatcccgtt  cttcgccatg  ggtcatggaa  ctaaaggagt   960

gtttgagctt  ctgtccggat  ggcggagaac  caaagagaac  ttgcccttca  aagacaggat  1020

agcagatgcc  tattctgatg  tgatggtcac  ctataccatg  accagctccc  tgtacttcat  1080

cacttttggc  atgggtgcca  gcccattcac  aaacatagag  gctgtgaagg  tcttctgtca  1140

aaacatgtgt  gtctctattc  tgttgaacta  cttctacatt  ttctccttct  ttggctcctg  1200

tctggtcttt  gctggccaac  tagagcaaaa  ccgctaccac  agcatctttt  gctgtaagat  1260

cccttctgca  gaatacctgg  atcgcaaacc  tgtgtggttc  cagacagtga  tgagtgatgg  1320

gcatcaacag  acgtccatc   atgagacgaa  ccccctaccag  caccacttca  ttcagcactt  1380

cctccgtgaa  cattataatg  aatggattac  caatatatat  gtgaagccat  ttgttgtcat  1440

cctctatctc  atttatgcct  ccttctcctt  catggggtgc  ttacagatca  gtgacgagc   1500

caacatcatc  aatctactag  ccagtgattc  gccaagtgtt  tcctatgcca  tggttcagca  1560

gaaatatttc  agcaactata  gccctgtgat  aggattctac  gtctatgagc  ccctagagta  1620

ctggaacagc  agcgtccagg  atgacctaag  aagactctgt  agtggattca  ctgcagtgtc  1680

ctgggtggag  cagtactacc  agttcctgaa  agtcagcaac  gtcagtgcca  ataacaaaag  1740

tgacttcatc  agtgtcctgc  aaagctcatt  tttaaaaaag  ccagaattcc  agcattttcg  1800

aaatgatatc  atcttctcca  aggcagggga  tgaaagcaat  atcattgctt  ctcgcttgta  1860

tctggtggcc  aggactagca  gagacaagca  gaaagaaatc  acagaagtgt  ggaaaagct   1920

gaggcccta   tccctctcaa  agagcatccg  attcatcgtg  ttcaacccct  cctttgtctt  1980

catgaccat   tacagcttgt  ctgtcacagt  gcctgttctg  attgcaggct  ttggtgttct  2040

cctggtgtta  atcctgactt  ttttcctagt  gatccaccct  ctgggaaact  tctggctaat  2100

tcttagcgtc  acctcaattg  agctgggcgt  tctgggctta  atgacattat  ggaacgtcga  2160

catggattgc  atttctatct  tgtgccttat  ctacaccttg  aatttcgcca  ttgaccactg  2220
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tgcaccactg cttttcacat ttgtattagc aactgagcac acccgaacac aatgtataaa    2280

aagctccttg caagaccatg ggacagccat tttgcaaaat gttacttctt ttcttattgg    2340

gttagtcccc cttctatttg tgccttcgaa cctgaccttc acactgttca aatgcttgct    2400

gctcactggg ggttgcacac ttctgcactg ttttgttatt ttacctgtgt tcctaacgtt    2460

tttccccccct tccaaaaagc accacaagaa aaagaaacgt gccaagcgaa aggagagaga    2520

ggaaattgaa tgcatagaaa ttcaagagaa cccggatcac gtcaccacag tatga        2575
```

```
<210> SEQ ID NO 621
<211> LENGTH: 829
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 621

Met Leu Arg Gln Val Leu Arg Arg Gly Leu Gln Ser Phe Cys His Arg
1               5                   10                  15

Leu Gly Leu Cys Val Ser Arg His Pro Val Phe Phe Leu Thr Val Pro
            20                  25                  30

Ala Val Leu Thr Ile Thr Phe Gly Leu Ser Ala Leu Asn Arg Phe Gln
        35                  40                  45

Pro Glu Gly Asp Leu Glu Arg Leu Val Ala Pro Ser His Ser Leu Ala
    50                  55                  60

Lys Ile Glu Arg Ser Leu Ala Ser Ser Leu Phe Pro Leu Asp Gln Ser
65                  70                  75                  80

Lys Ser Gln Leu Tyr Ser Asp Leu His Thr Pro Gly Arg Tyr Gly Arg
                85                  90                  95

Val Ile Leu Leu Ser Pro Thr Gly Asp Asn Ile Leu Leu Gln Ala Glu
            100                 105                 110

Gly Ile Leu Gln Thr His Arg Ala Val Leu Glu Met Lys Asp Gly Arg
            115                 120                 125

Asn Ser Phe Ile Gly His Gln Leu Gly Gly Val Val Glu Val Pro Asn
        130                 135                 140

Ser Lys Asp Gln Arg Val Lys Ser Ala Arg Ala Ile Gln Ile Thr Tyr
145                 150                 155                 160

Tyr Leu Gln Thr Tyr Gly Ser Ala Thr Gln Asp Leu Ile Gly Glu Lys
                165                 170                 175

Trp Glu Asn Glu Phe Cys Lys Leu Ile Arg Lys Leu Gln Glu Glu His
            180                 185                 190

Gln Glu Leu Gln Leu Tyr Ser Leu Ala Ser Phe Ser Leu Trp Arg Asp
            195                 200                 205

Phe His Lys Thr Ser Ile Leu Ala Arg Ser Lys Val Leu Val Ser Leu
        210                 215                 220

Val Leu Ile Leu Thr Thr Ala Thr Leu Ser Ser Ser Met Lys Asp Cys
225                 230                 235                 240

Leu Arg Ser Lys Pro Phe Leu Gly Leu Leu Gly Val Leu Thr Val Cys
                245                 250                 255

Ile Ser Ile Ile Thr Ala Ala Gly Ile Phe Phe Ile Thr Asp Gly Lys
            260                 265                 270

Tyr Asn Ser Thr Leu Leu Gly Ile Pro Phe Phe Ala Met Gly His Gly
            275                 280                 285

Thr Lys Gly Val Phe Glu Leu Leu Ser Gly Trp Arg Arg Thr Lys Glu
        290                 295                 300

Asn Leu Pro Phe Lys Asp Arg Ile Ala Asp Ala Tyr Ser Asp Val Met
305                 310                 315                 320
```

```
Val Thr Tyr Thr Met Thr Ser Ser Leu Tyr Phe Ile Thr Phe Gly Met
            325                 330                 335

Gly Ala Ser Pro Phe Thr Asn Ile Glu Ala Val Lys Val Phe Cys Gln
            340                 345                 350

Asn Met Cys Val Ser Ile Leu Leu Asn Tyr Phe Tyr Ile Phe Ser Phe
            355                 360                 365

Phe Gly Ser Cys Leu Val Phe Ala Gly Gln Leu Glu Gln Asn Arg Tyr
    370                 375                 380

His Ser Ile Phe Cys Cys Lys Ile Pro Ser Ala Glu Tyr Leu Asp Arg
385                 390                 395                 400

Lys Pro Val Trp Phe Gln Thr Val Met Ser Asp Gly His Gln Gln Thr
                405                 410                 415

Ser His His Glu Thr Asn Pro Tyr Gln His His Phe Ile Gln His Phe
            420                 425                 430

Leu Arg Glu His Tyr Asn Glu Trp Ile Thr Asn Ile Tyr Val Lys Pro
            435                 440                 445

Phe Val Val Ile Leu Tyr Leu Ile Tyr Ala Ser Phe Ser Phe Met Gly
    450                 455                 460

Cys Leu Gln Ile Ser Asp Gly Ala Asn Ile Ile Asn Leu Leu Ala Ser
465                 470                 475                 480

Asp Ser Pro Ser Val Ser Tyr Ala Met Val Gln Gln Lys Tyr Phe Ser
                485                 490                 495

Asn Tyr Ser Pro Val Ile Gly Phe Tyr Val Tyr Glu Pro Leu Glu Tyr
            500                 505                 510

Trp Asn Ser Ser Val Gln Asp Asp Leu Arg Arg Leu Cys Ser Gly Phe
            515                 520                 525

Thr Ala Val Ser Trp Val Glu Gln Tyr Tyr Gln Phe Leu Lys Val Ser
    530                 535                 540

Asn Val Ser Ala Asn Asn Lys Ser Asp Phe Ile Ser Val Leu Gln Ser
545                 550                 555                 560

Ser Phe Leu Lys Lys Pro Glu Phe Gln His Phe Arg Asn Asp Ile Ile
                565                 570                 575

Phe Ser Lys Ala Gly Asp Glu Ser Asn Ile Ile Ala Ser Arg Leu Tyr
            580                 585                 590

Leu Val Ala Arg Thr Ser Arg Asp Lys Gln Lys Glu Ile Thr Glu Val
            595                 600                 605

Leu Glu Lys Leu Arg Pro Leu Ser Leu Ser Lys Ser Ile Arg Phe Ile
    610                 615                 620

Val Phe Asn Pro Ser Phe Val Phe Met Asp His Tyr Ser Leu Ser Val
625                 630                 635                 640

Thr Val Pro Val Leu Ile Ala Gly Phe Gly Val Leu Leu Val Leu Ile
                645                 650                 655

Leu Thr Phe Phe Leu Val Ile His Pro Leu Gly Asn Phe Trp Leu Ile
            660                 665                 670

Leu Ser Val Thr Ser Ile Glu Leu Gly Val Leu Gly Leu Met Thr Leu
            675                 680                 685

Trp Asn Val Asp Met Asp Cys Ile Ser Ile Leu Cys Leu Ile Tyr Thr
    690                 695                 700

Leu Asn Phe Ala Ile Asp His Cys Ala Pro Leu Leu Phe Thr Phe Val
705                 710                 715                 720

Leu Ala Thr Glu His Thr Arg Thr Gln Cys Ile Lys Ser Ser Leu Gln
                725                 730                 735
```

-continued

```
Asp His Gly Thr Ala Ile Leu Gln Asn Val Thr Ser Phe Leu Ile Gly
            740                 745                 750

Leu Val Pro Leu Leu Phe Val Pro Ser Asn Leu Thr Phe Thr Leu Phe
        755                 760                 765

Lys Cys Leu Leu Leu Thr Gly Gly Cys Thr Leu Leu His Cys Phe Val
    770                 775                 780

Ile Leu Pro Val Phe Leu Thr Phe Phe Pro Pro Ser Lys Lys His His
785                 790                 795                 800

Lys Lys Lys Lys Arg Ala Lys Arg Lys Glu Arg Glu Glu Ile Glu Cys
            805                 810                 815

Ile Glu Ile Gln Glu Asn Pro Asp His Val Thr Thr Val
            820                 825
```

<210> SEQ ID NO 622
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 622

```
cagctctact ctttagcatc c                                              21
```

<210> SEQ ID NO 623
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 623

```
cctttagttc catgacccat g                                              21
```

<210> SEQ ID NO 624
<211> LENGTH: 6035
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 624

```
ggcggcggcg gcggcggccc cgggcgctga gcgggtgccc ggcgcggaga gcggcgagcg    60

cagccatgcc ccaggccgcc tccggggcag cagcagcggc ggccggggcc gaggcgcggg   120

ccggggcgc cggggggccg gcggcggccc gggcgggacg atgaagcggc agaacgtgcg    180

cacgctggcg ctcatcgtgt gcaccttcac ctacctgctg gtgggcgccg cggtcttcga    240

cgcgctggag tcggagcccg agctgatcga gcggcagcgg ctggagctgc ggcagcagga    300

gctgcgggcg cgctacaacc tcagccaggg cggctacgag gagctggagc gcgtcgtgct    360

gcgcctcaag ccgcacaagg ccggcgtgca gtggcgcttc gccggctcct tctacttcgc    420

catcaccgtc atcaccacca tcggctacgg gcacgcggcg cccagcacgg atggcggcaa    480

ggtgttctgc atgttctacg cgctgctggg catcccgctc acgctcgtca tgttccagag    540

cctgggcgag cgcatcaaca cccttggtga gtacctgctg caccgcgcca agaagggct    600

gggcatctcg tggccttcgc ttcgtctcat ccttacgggc ctcacggtca tcggcgcctt    660

cctcaacctc gtggtgctgc gcttcatgac catgaacgcc gaggacgaga gcgcgacgc    720

cgagcaccgc gcgctgctca cgcgcaacgg gcaggcgggc ggcggcggag ggagtggcag    780

cgcgcacact acggacaccg cctcatccac ggcggcagcg ggcggcgcg gcttccgcaa    840
```

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```
cgtctacgcg gaggtgctgc acttccagtc catgtgctcg tgcctgtggt acaagagccg      900

cgagaagctg cagtactcca tccccatgat catcccgcgg gacctctcca cgtccgacac      960

gtgcgtggag cagagccact cgtcgccggg aggggcggc cgctacagcg acacgccctc      1020

gcgacgctgc ctgtgcagcg gggcgccacg ctccgccatc agctcggtgt ccacgggtct      1080

gcacagcctg tccaccttcc gcggactcat gaagcgcagg agctccgtgt gactgccccg      1140

aggggcctgg agcacctggg ggcgcgggcg ggggaccccт gctgggaggc caggagactg      1200

cccctgctgc cttctgccca gtgggacccc gcacaacatc cctcaccact ctcccccagc      1260

accccatct ccgactgtgc ctgcttgcac cagccggcag gaggccgggc tctgaggacc       1320

cctggggccc ccatcggagc cctgcaaatt ccgagaaatg tgaaacttgg tggggtcagg      1380

gaggaaaggc agaagctggg agcctccctt ccctttgaaa atctaagaag ctcccagtcc      1440

tcagagaccc tgctggtacc cagaccccca ccttcggagg ggacttcatg ttccgtgtac      1500

gtttgcatct ctatttatac ctctgtcctg ctaggtctcc caccttccct tggttccaaa      1560

agccagggtg tctttgtcca agtcacccct actcagcccc actcccttтc ctcatcccca      1620

gctgtgtctc ccaacctccc ttcgtgttgt tttgcatggc tttgcagtta tggagaaagt      1680

ggaaacccag cagtccctaa agctggtccc cagaaagcag gacagaaaga aggagggaca      1740

ggcaggcagc aggaggggcg agctgggagg caggaggcag cggcctgtca gtctgcagaa      1800

tggtcgcact ggaggttcaa gctaactggc ctccagccac attctcatag caggtaggac      1860

ttcagccttc cagacactgc ccttagaatc tggaacagaa gacttcagac tcaccataat      1920

tgctgataat tacctactct taaatttgtc gagtgatttt tagcctctga aaactctatg      1980

ctggccactg attcctttga gtctcacaaa accctactta ggtcatcagg gcaggagttc      2040

tcactcccat tttacagatg agaatactga ggcctggaca ggtgaagtga ccagagagca      2100

aaaggcaaag gggtggggc tgggtgcagt ggctcacacc tgtattccca cacttttgg       2160

aggctgaggt tagaggattg cttgagccca ggaattcgag accagcctag gcgacatagt      2220

gagaccccat ctctacaaaa aataaaaaat ttaccaggtg tggtggcacg tgcctgggag      2280

tcccagcgac ttgggaggct gaggtgggag gattgtttga gcctgggagg tcaaggctgt      2340

agtgagccct gattacacca ctgtactcca gcctgggtga cagggcaaga ccctgtctca      2400

aaaaaaaaaa aaaatggca aagggagaca agagcccagc ctacttgttc ctagccaaag      2460

tgttctttcc ttccagcttg gcctgctctt aaaagcaaag ctcctgcagt gtacatcctg      2520

gcattgtgtg gctacctggg ttttaaacca gaatcagaag tcccgggtca gagggcactg      2580

ctgaggctca gcctcttctc ttcttggcca ggaggcagca gctctgaatg ggcccctgag      2640

gctgcacagg ggcctttgtc actggggtgc atgcttacaa acagtgcagt tcttggcacc      2700

gaggtaagca gggctgggtc tcatggcaga aaggccagga tctggggctc taggaatttg      2760

ggaattgggc agagtggcca agaaagctgg caggcatatc ctatgggaca tcacacctgg      2820

caccattgtc attgttggtg cctgtgtccc aagtagctag tgataagctg aggctgcagc      2880

aagaaacacc cttcccaggt gggggagttt ggaccagagg tgccctctgc ccaccacacc      2940

tgcaacccag aagcccagat ggaacgcagc tgatgaaggt gatgcttgag gctcactttt      3000

ggggcccac agctggagcc ggtatagtga ctgggacaac atcaaggggt ggatgagggg        3060

cctctcctcc cgcaacactg ccttcccatg ctgttcccct gccagctcct taacactgcc      3120

gaccaaggcc agacctggca ttcaggaaag ttggagggca gcaccatag ggtggccagc       3180
```

```
ctcaggcccc accccagctg tgtcctctag tctctgggga cccctggggg gaagaagtct   3240

accctgcttg tgagtcccgt ctcagtgtgg aggaactggc tgcacgtggg acctgaaggt   3300

gccctctgtg tttatgttgg ggggggggg gcagtgctgg ctgcctctgt cctgtgtgtg   3360

accctgccct cgaagggtcc tgtcctgtca gtcccgaggg agccacaacc aaagctgcgg   3420

agagaaggtg gggaacggtg cggagtggcc gtggggcaca gcgtggcaga ctgttcagtc   3480

tctgctgggt ctttcctagg gacctggaag gccagtgttg cttcccctc actccctttc     3540

actgcaggca gcctctctcc ttccccaatg ccttatgcct gggcacactg ccacagaata   3600

tgcaatatgt gtgggtgacg atgccctcac gaccacaccc ccaccccggg cagccccgg     3660

actccaaagg tcgtggctgc cacagcctcc ctcagctctt cctgcctatc tgtcttcaca   3720

ctgagaatgg cgcccaataa atgctatcca cggagaccag gctcaggctc cagctgcctc   3780

tgtcatcgta tgcccttgct gctgccaggg aggggccatc tcccaccccc tccctgccg     3840

gggtctacaa acatacctag ctgctgggtg ccgtggctca cacctataat cacagcacta   3900

ggcgggcaga tcacctgagg tcagaagttc aagaccagcc tggccaacat ggtaaaaccc   3960

cgtctctact aaaaatacaa aaattagctg agcgtggtgg cgcctgtctg tagtcccagc   4020

tactcggcta ctcaggaggc tgacgcacga gaatcgcttg aacccgggag gcggaggttg   4080

cagtgagctg agatcgcgcc actgcactcc agcctgagcg atagagtgag accctgtcta   4140

aaaaaaacaa taataataaa ataaaataac atacctagct gactcgccat gggctcgctg   4200

gcctgtgggc gacactggct tccctttttgg gatttcccag aagatccaga ttttcttaag   4260

tccccttgga acagactaag aaagaaacac cttagaaatc acctggtcct attgtcccc    4320

cgtacatgag taactgaggc ccacagagag caaatcgcct gcctgagtca cacagcagtg   4380

agtggcagac ctaggctagg aactagaact ggggattgct attccagtgc tccccatcct   4440

cacacagcct gtggagtccg cctggacaca ccccagctga cagtggtacc tcccagtcag   4500

ccaggagaat ggattccttc tcctgcagta ggggcccct ggctgagtgg cctgattgac     4560

taaaacatat gtctttgaag gagagtgcat cacaagcacc tttctttggg gtagattttt   4620

ctctgggtct agagggacac ctcaggcttg ggactgggcc tcagaaccta ggacagaccc   4680

tgagagcaga cccaccttat ccatctggtg ccagctcccc aggtcagcta cagcaacccc   4740

cgaacttcat agagtacaat ccacagtaat agcacacagc tctgtaccta tctagctcca   4800

tgcctatcta tctgcctacc tttcacaaaa taattcttag caaccctgct acagccaatg   4860

attctaatac gttctgttct attacatgtt ataaatgct ggtcacgatc cactaaattg     4920

atgtctctac ctgctaatgg tttaatacct gcagattgaa atatactgga gaaataaaga   4980

gagtaggagt agggacactt tctcccagtg cccacaccgc ccctcgttac ccgcataggt   5040

caactgaaag atacagagag ggaagctttg atggggggtt cagagttcaa aggaagaaat   5100

gatggcacct gcactccctg cccccagagg caggacacag ccagccctcc tgtgacagca   5160

ctcctggcag ctccttgttg gcctgcagcc cttagttgcc attgactcac ccactcctaa   5220

ggccaccaca tcaaaatctg aggcttactg ccctggccca cctgcctctg tctttcttaa   5280

aacagctaaa tgcaacgata gcagaaatta gcttgttttt gaggttggca atgaccagtt   5340

caactcttat tttcttaagc agtgcttgca ggacataaat gtgatgacac ttgccctcct   5400

ttctttatcg cctggggcag actttacaaa cagacctggg aggagtcccc taaggggctg   5460

catttatccc catctcccta gggggtgatca gcattgtgac agctgggcag agcagtggtg   5520

aactgcaccc atgtccctgc tcacatctcc taagatctca gaattgcctg aggttctagc   5580
```

```
gtgggctcct tctctccaga tgatgccatc cccacccccc tcatttccac acagcatctg    5640

aggcatcctg cactaaaaga tatatgtaca gcaaaacaaa aatagaaaac cagcacagca    5700

gagtggaggt ggggtataaa tatacccaga tccccgctga tttggttact cggggtgagc    5760

atcagatgga aatagaagtt tccggggggcc aagagagaaa gagggatgta acgacaattc    5820

ttttcaaaac gtgtcccatg gtatgcctcg tggaaaaaat ggttcgttgg tcaaatgaat    5880

ttgggaaaat gctgtcaata tcaccgactc atggagcttc gcaaggcatc ttagcttaat    5940

aaaggttatg aaaagtcttg cagcaaagat gctgtttacc ccacttaatc cagcactgcc    6000

caaactcatt ccaaatacca gagcctctgt ttgca                               6035
```

<210> SEQ ID NO 625
<211> LENGTH: 323
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 625

```
Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe
1               5                   10                  15

Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
            20                  25                  30

Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu
        35                  40                  45

Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
    50                  55                  60

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
65                  70                  75                  80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
                85                  90                  95

Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
            100                 105                 110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
        115                 120                 125

Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
    130                 135                 140

Lys Gly Leu Gly Ile Ser Trp Pro Ser Leu Arg Leu Ile Leu Thr Gly
145                 150                 155                 160

Leu Thr Val Ile Gly Ala Phe Leu Asn Leu Val Val Leu Arg Phe Met
                165                 170                 175

Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu
            180                 185                 190

Leu Thr Arg Asn Gly Gln Ala Gly Gly Gly Gly Ser Gly Ser Ala
        195                 200                 205

His Thr Thr Asp Thr Ala Ser Ser Thr Ala Ala Ala Gly Gly Gly Gly
    210                 215                 220

Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met Cys Ser
225                 230                 235                 240

Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile Pro Met
                245                 250                 255

Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu Gln Ser
            260                 265                 270

His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro Ser Arg
        275                 280                 285
```

-continued

Arg Cys Leu Cys Ser Gly Ala Pro Arg Ser Ala Ile Ser Ser Val Ser
    290   295   300

Thr Gly Leu His Ser Leu Ser Thr Phe Arg Gly Leu Met Lys Arg Arg
305   310   315   320

Ser Ser Val

<210> SEQ ID NO 626
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 626

agactttaca aacagacctg g   21

<210> SEQ ID NO 627
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 627

gcttgcagga cataaatgtg atg   23

<210> SEQ ID NO 628
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 628

tgacactggc aaaacaatgc a   21

<210> SEQ ID NO 629
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence:
      Oligonucleotide

<400> SEQUENCE: 629

ggtcctttc accagcaagc t   21

<210> SEQ ID NO 630
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: siRNA

<400> SEQUENCE: 630

ccacagaagg uaccaguuau u   21

<210> SEQ ID NO 631
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: siRNA

```
<400> SEQUENCE: 631

uaacugguac cuucuguggu u                                                      21


<210> SEQ ID NO 632
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: siRNA

<400> SEQUENCE: 632

cagcaagacu cccucuaaau u                                                      21


<210> SEQ ID NO 633
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: siRNA

<400> SEQUENCE: 633

uuuagaggga gucuugcugu u                                                      21


<210> SEQ ID NO 634
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: target RNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 634

nnccacagaa gguaccaguu a                                                      21


<210> SEQ ID NO 635
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence: target RNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 635

nncagcaaga cucccucuaa a                                                      21


<210> SEQ ID NO 636
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(4)
<223> OTHER INFORMATION: Xaa is any amino acid

<400> SEQUENCE: 636

Cys Cys Xaa Xaa Cys Cys
1               5
```

The invention claimed is:

1. A method of diagnosing or monitoring ovarian cancer, wherein the method comprises the steps of:

detecting the presence of or determining the quantity of a tumor-associated nucleic acid in a biological sample comprising ovarian tissue isolated from a human patient having or suspected of having ovarian cancer, and

diagnosing or monitoring ovarian cancer based on the presence or quantity of the tumor-associated nucleic acid in the biological sample, wherein

the tumor-associated nucleic acid is selected from the group consisting of (a) a nucleic acid that comprises a nucleic acid sequence consisting essentially of SEQ ID NO: 553, and (b) a nucleic acid that has at least 90% sequence identity with the nucleic acid of (a);

the detecting or determining comprises (i) contacting the biological sample with an agent that binds specifically to the tumor-associated nucleic acid, and (ii) detecting the formation of or determining the quantity of a complex between the agent and the tumor-associated nucleic acid wherein said agent is an oliqonucleotide or polynucleotide that hybridizes specifically to the tumor-associated nucleic acid or to the complementary nucleic acid sequence, and has a nucleic acid sequence comprising SEQ ID NO: 555 or 556; and

the ovarian cancer that is characterized by expression of or abnormal expression of a tumor-associated antigen encoded by the tumor-associated nucleic acid.

2. The method of claim 1, wherein the monitoring of the ovarian cancer comprises determining regression, course or onset of the ovarian cancer in the patient.

3. The method of claim 1, wherein the method comprises a detection of the presence of or a determination of the quantity of the tumor-associated nucleic acid in a first sample at a first point in time and in a further sample at a second point in time and a comparison of the presence of or quantity of the tumor-associated nucleic acid in the two samples.

4. The method of claim 1, wherein the agent is labeled in a detectable manner.

5. The method of claim 1, wherein the ovarian tissue is from a tissue biopsy.

6. The method of claim 1, wherein the tumor-associated antigen comprises an amino acid sequence consisting essentially of SEQ ID NO: 554.

7. A method of diagnosing or monitoring ovarian cancer, wherein the method comprises the steps of:

detecting or determining the quantity of a tumor-associated nucleic acid in a biological sample comprising ovarian tissue isolated from a human patient having or suspected of having ovarian cancer, and

diagnosing or monitoring ovarian cancer based on the presence or quantity of the tumor-associated nucleic acid in the biological sample, wherein

the tumor-associated nucleic acid is selected from the group consisting of (a) a nucleic acid that comprises a nucleic acid sequence consisting essentially of SEQ ID NO: 553, and (b) a nucleic acid that has at least 90% sequence identity with the nucleic acid of (a);

the detecting or determining comprises (i) contacting the biological sample with an agent that binds specifically to the tumor-associated nucleic acid, and (ii) detecting the formation of or determining the quantity of a complex between the agent and the tumor-associated nucleic acid via real-time reverse-transcription polymerase chain reaction (RT-PCR);

the ovarian cancer is characterized by expression or abnormal expression of a tumor-associated antigen encoded by the tumor-associated nucleic acid; and

the agent is an oligonucleotide or polynucleotide that hybridizes specifically to the tumor-associated nucleic acid or to the complementary nucleic acid sequence, and has a nucleic acid sequence comprising SEQ ID NO: 555 or 556.

8. The method of claim 7, wherein the monitoring of the ovarian cancer comprises determining regression, course or onset of the ovarian cancer in the patient.

9. The method of claim 7, wherein the method comprises a detection of the presence of or determination of the quantity of the tumor-associated nucleic acid in a first sample at a first point in time and in a further sample at a second point in time and a comparison of the presence of or quantity of the tumor-associated nucleic acid in the two samples.

10. The method of claim 7, wherein the agent is labeled in a detectable manner.

11. The method of claim 7, wherein the ovarian tissue is from a tissue biopsy.

12. The method of claim 7, wherein the tumor-associated antigen comprises an amino acid sequence consisting essentially of SEQ ID NO: 554.

13. The method of claim 7, wherein the agent is an oligonucleotide or polynucleotide that hybridizes specifically to the tumor-associated nucleic acid and has a nucleic acid sequence comprising SEQ ID NO: 555.

14. The method of claim 7, wherein the agent is an oligonucleotide or polynucleotide that hybridizes specifically to the tumor-associated nucleic acid and has a nucleic acid sequence comprising SEQ ID NO: 556.

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